

82028

From: Salimi, Ali  
Sent: Tuesday, December 10, 2002 1:52 PM  
To: STIC-Biotech/ChemLib  
Subject: 09/701,080

Can you please conduct a search for the application serial no. 09/701,080, including interference search for the following sequences:

SEQ ID NO: 1, and 18

Thanks!

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Edward Hart  
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STIC/Biotech  
CMI 6B02 Tel: 305-9203

Searcher: \_\_\_\_\_  
Phone: \_\_\_\_\_  
Location: \_\_\_\_\_  
Date Picked Up: 12/13/02  
Date Completed: 12/13/02  
Searcher Prep/Review: \_\_\_\_\_  
Clerical: \_\_\_\_\_  
Online time: \_\_\_\_\_

TYPE OF SEARCH:  
NA Sequences: \_\_\_\_\_  
AA Sequences: 2  
Structures: \_\_\_\_\_  
Bibliographic: \_\_\_\_\_  
Litigation: \_\_\_\_\_  
Full text: \_\_\_\_\_  
Patent Family: \_\_\_\_\_  
Other: \_\_\_\_\_

VENDOR/COST (where applic.)  
STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
Questel/Orbit: \_\_\_\_\_  
DRLink: \_\_\_\_\_  
Lexis/Nexis: \_\_\_\_\_  
Sequence Sys.: 02  
WWW/Internet: \_\_\_\_\_  
Other (specify): \_\_\_\_\_

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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:20 ; Search time 21.3067 Seconds  
(without alignments)  
208.519 Million cell updates/sec

Title: US-09-701-080C-18  
Perfect score: 851  
Sequence: 1 MFQDPQERRKRLPQLCTELQ.....WTGRCSGCRSSRRTRRQL 151

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues  
Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	162	1	US-08-316-239B-3
2	843	99.1	266	3	US-08-860-165-10
3	843	99.1	266	4	US-09-359-382-10
4	843	99.1	266	4	US-09-367-309A-1
5	843	99.1	273	4	US-09-485-885-4
6	843	99.1	292	4	US-09-485-885-10
7	843	99.1	371	4	US-09-485-885-6
8	843	99.1	390	4	US-09-485-885-14
9	840	98.7	162	3	US-08-316-239B-4
10	539	63.3	172	3	US-08-860-165-12
11	539	63.3	172	4	US-09-359-382-12
12	487	57.2	172	3	US-08-860-165-14
13	487	57.2	172	4	US-09-359-382-14
14	479	56.3	182	1	US-08-117-083-10
15	469.5	55.2	158	2	US-08-247-904B-10
16	469.5	55.2	158	3	US-08-767-942A-19
17	469.5	55.2	271	1	US-08-117-083-14
18	469.5	55.2	278	4	US-09-485-885-21
19	469.5	55.2	383	4	US-09-485-885-23
20	320	37.6	375	4	US-09-000-094-22
21	320	37.6	465	4	US-09-000-094-24
22	320	37.6	1587	4	US-09-000-094-46
23	320	37.6	30	1	US-08-363-586-4
24	163	19.2	21	2	US-08-934-915-167
25	120	14.1	20	2	US-08-934-915-165
26	115	13.5	21	2	US-08-934-915-166
27	115	13.5	21	2	US-08-934-915-166

28	115	13.5	32	1	US-08-466-285-2	Sequence 2, Appl
29	115	13.5	32	4	US-08-164-768-2	Sequence 2, Appl
30	109	12.8	30	2	US-08-934-915-45	Sequence 45, Appl
31	107	12.6	20	2	US-08-934-915-44	Sequence 44, Appl
32	107	12.6	20	2	US-08-934-915-163	Sequence 163, App
33	104	12.2	20	2	US-08-934-915-164	Sequence 164, App
34	98	11.5	20	2	US-08-934-915-159	Sequence 159, App
35	98	11.5	20	2	US-08-934-915-162	Sequence 162, App
36	97	11.4	20	2	US-08-934-915-160	Sequence 160, App
37	97	11.4	20	2	US-08-934-915-161	Sequence 161, App
38	96	11.3	32	1	US-08-466-285-4	Sequence 4, Appl
39	96	11.3	32	4	US-08-164-768-4	Sequence 4, Appl
40	90	10.6	23	1	US-08-363-586-3	Sequence 3, Appl
41	85	10.0	15	1	US-07-909-122-2	Sequence 2, Appl
42	85	10.0	591	2	US-08-889-402-1	Sequence 1, Appl
43	85	10.0	605	2	US-08-889-402-2	Sequence 2, Appl
44	82	9.6	15	4	US-08-075-541D-52	Sequence 52, Appl
45	80.5	9.5	256	4	US-08-804-166-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1  
US-08-316-239B-3  
; Sequence 3, Application US/08316239B  
; Patent No. 5679509  
; GENERAL INFORMATION:  
; APPLICANT: Wheeler, Cosette M.  
; TITLE OF INVENTION: Parmenter, Cheryl A.  
; TITLE OF INVENTION: Methods and a diagnostic Aid for  
; TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
; TITLE OF INVENTION: Increased Risk of Developing Cervical Cancer  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Jagtiani & Associates  
; STREET: 6126 Rocky Way Court  
; CITY: Centerville  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 20120-3400  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/316,239B  
; FILING DATE: 30-SEP-1994  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jagtiani, Ajay A.  
; REGISTRATION NUMBER: 35,205  
; REFERENCE/DOCKET NUMBER: UNNE-0001  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 817-9453  
; TELEFAX: (703) 803-9387  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 162 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: not relevant  
; TOPOLOGY: not relevant  
; MOLECULE TYPE: protein  
; ; HYPOTHETICAL: NO  
; ;  
; US-08-316-239B-3  
Query Match 99.1%; Score 843; DB 1; Length 162;  
Best Local Similarity 99.3%; Pred. No. 2.8e-82;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 1 MFQDPQERRKRLPQLCTELQTHIHILIECVYCKQQLLRREYDFAFRDLCLVYRDGNPY 60

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Db      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
      61 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
      68 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151
      128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158

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RESULT 2
US-08-860-165-10
; Sequence 10, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; CURRENT FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PNO157
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-10

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Query Match
Best Local Similarity 99.1%; Score 843; DB 3; Length 266;
Matches 150; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
Db      61 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
      68 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151
      128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158

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RESULT 3
US-09-359-382-10
; Sequence 10, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20

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; EARLIER APPLICATION NUMBER: AU PNO157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 10
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Human papillomavirus type 16
US-09-359-382-10

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Query Match
Best Local Similarity 99.1%; Score 843; DB 4; Length 266;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
Db      61 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
      68 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151
      128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158

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RESULT 4
US-09-367-309A-1
; Sequence 1, Application US/09367309A
; Patent No. 6428807
; GENERAL INFORMATION:
; APPLICANT: MACFARLAN, RODERICK I.
; APPLICANT: MALLIAROS, JIM
; TITLE OF INVENTION: CHELATING IMMUNOSTIMULATING COMPLEXES
; FILE REFERENCE: 017227/0149
; CURRENT APPLICATION NUMBER: US/09/367,309A
; CURRENT FILING DATE: 1999-08-11
; PRIOR APPLICATION NUMBER: PCT/AU98/00080
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: AU PO 5178
; PRIOR FILING DATE: 1997-02-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 1
; LENGTH: 266
; TYPE: PRF
; ORGANISM: Human papillomavirus type 16
US-09-367-309A-1

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Query Match
Best Local Similarity 99.1%; Score 843; DB 4; Length 266;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY      1 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 60
      8 MFODPOERPRKLPOLCTELQTTIHDIILECVYCKQOLLREVVDFAFRDLCIYRDGNPY 67
Db      61 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120
      68 AVCDKCLKEFSKYSERYHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 127
QY      121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151
      128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158

```

```

RESULT 5
US-09-485-885-4
; Sequence 4, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine

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; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-4

Query Match
Query Local Similarity 99.1%; Score 843; DB 4; Length 273;
Best Local Similarity 99.3%; Pred. No. 5e-82; 1; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 1;
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QY 1 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 60
DB 114 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 173
QY 61 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 120
DB 174 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 233
QY 121 KQRFHNIRGRTGRCMSCRSSRTRRETOL 151
DB 234 KQRFHNIRGRTGRCMSCRSSRTRRETOL 264
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RESULT 6
US-09-485-885-10
; Sequence 10, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-10
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Query Match
Query Local Similarity 99.1%; Score 843; DB 4; Length 292;
Best Local Similarity 99.3%; Pred. No. 5.4e-82; 1; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 60
DB 133 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 192
QY 61 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 120
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DB 193 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 252
QY 121 KQRFHNIRGRTGRCMSCRSSRTRRETOL 151
DB 253 KQRFHNIRGRTGRCMSCRSSRTRRETOL 283
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RESULT 7
US-09-485-885-6
; Sequence 6, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-485-885-6
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Query Match
Query Local Similarity 99.1%; Score 843; DB 4; Length 371;
Best Local Similarity 99.3%; Pred. No. 7.1e-82; 1; Indels 0; Gaps 0;
Matches 150; Conservative 0; Mismatches 1;
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QY 1 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 60
DB 114 MFODDERRKLPLCTELQTTIHDIIECYCKOOLLREYVDFAFRLCTIVYRDGNPY 173
QY 61 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 120
DB 174 AVCDKCLKFKYSKISEYRHVCSLYGTTLEQYNNKPLCDLLIRINCQKPLCEPEKORHLD 233
QY 121 KQRFHNIRGRTGRCMSCRSSRTRRETOL 151
DB 234 KQRFHNIRGRTGRCMSCRSSRTRRETOL 264
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```

RESULT 8
US-09-485-885-14
; Sequence 14, Application US/09485885
; Patent No. 6342224
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabazon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/09/485,885
; CURRENT FILING DATE: 2000-02-18
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 14
; LENGTH: 390
; TYPE: PRT
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; ORGANISM: Homo sapien  
US-09-485-885-14

Query Match  
Best Local Similarity 99.1%; Score 843; DB 4; Length 390;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGNGPY 60  
DB 133 MFODPOERPKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGNGPY 192  
QY 61 AVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 120  
DB 193 AVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 252  
QY 121 KROFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 253 KROFHNIRGRWTRGCMSCCRSSRTRETOL 283

## RESULT 9

US-08-316-239B-4  
; Sequence 4, Application US/08316239B  
; Patent No. 5679509

GENERAL INFORMATION:  
APPLICANT: Wheeler, Cosette M.  
TITLE OF INVENTION: Methods and a Diagnostic Aid for  
TITLE OF INVENTION: Distinguishing a Subset of HPV that is Associated with an  
TITLE OF INVENTION: Increased Risk of Developing Cervical Dysplasia and  
NUMBER OF INVENTIONS: 4  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Jagtiani & Associates  
STREET: 6126 Rocky Way Court  
CITY: Centreville  
STATE: VA  
COUNTRY: USA  
ZIP: 20120-3400  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/316,239B  
FILING DATE: 30-SEP-1994  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Jagtiani, Ajay A.  
REGISTRATION NUMBER: 35,205  
REFERENCE/DOCKET NUMBER: UNME-0001  
TELEPHONE: (703) 817-9453  
TELEFAX: (703) 803-9387  
INFORMATION FOR SEQ. ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 162 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: not relevant  
MOLECULE TYPE: protein  
HYPOTHEICAL: NO  
US-08-316-239B-4

Query Match  
Best Local Similarity 98.7%; Score 840; DB 1; Length 162;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGNGPY 60  
DB 8 MFODPOERPKLPOLCTELQTTIHDIIECVYCKOQLLRREYVDFAFRDLCIYRGNGPY 67

QY 61 AVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 120  
DB 68 AVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKORHLD 127  
QY 121 KROFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 128 KROFHNIRGRWTRGCMSCCRSSRTRETOL 158

## RESULT 10

US-08-860-165-12  
; Sequence 12, Application US/08860165A  
; Patent No. 6004557

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 17227/130  
CURRENT APPLICATION NUMBER: US/08/860,165A  
EARLIER FILING DATE: 1997-09-22  
CURRENT APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PNO157  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 15  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO: 12  
LENGTH: 172  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion  
US-08-860-165-12

Query Match  
Best Local Similarity 98.3%; Score 539; DB 3; Length 172;  
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 GNPYAVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKOR 116  
DB 2 GNPYAVCDCKLKFYSKISEYRHVYSLYGTTLLEQYKPKLDDLIRINCOKPLCPPEKOR 61  
QY 117 RHLDKKORFHNIRGRWTRGCMSCCRSSRTRETOL 151  
DB 62 RHLDKKORFHNIRGRWTRGCMSCCRSSRTRETOL 96

## RESULT 11

US-09-359-382-12  
; Sequence 12, Application US/09359382  
; Patent No. 6306397

GENERAL INFORMATION:  
APPLICANT: EDWARDS, Stirling John  
APPLICANT: COX, John Cooper  
APPLICANT: WEBB, Elizabeth Ann  
APPLICANT: FRAZER, Ian  
TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS  
FILE REFERENCE: 017227/0148  
CURRENT APPLICATION NUMBER: US/09/359,382  
EARLIER FILING DATE: 1999-07-23  
EARLIER APPLICATION NUMBER: US 08/860,165  
EARLIER FILING DATE: 1997-09-22  
EARLIER APPLICATION NUMBER: PCT/AU95/00868  
EARLIER FILING DATE: 1995-12-20  
EARLIER APPLICATION NUMBER: AU PNO157/94  
EARLIER FILING DATE: 1994-12-20  
NUMBER OF SEQ ID NOS: 27  
SOFTWARE: Patentln Ver. 2.0  
SEQ ID NO: 12  
LENGTH: 172  
TYPE: PRT

```
; ORGANISM: Human papillomavirus type 16
US-09-359-382-12

Query Match          63.3%; Score 539; DB 4; Length 172;
Best Local Similarity 98.9%; Pred. No. 5.9e-50;
Matches 94; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 57 GNPYAVCDKCLKFKYSKYSEYRHVCYSLYGTTLLEQOYNKPLCDLLIRNCINQKPLCEPKO 116
      |||
DB 2 GNPYAVCDKCLKFKYSKYSEYRHVCYSLYGTTLLEQOYNKPLCDLLIRNCINQKPLCEPKO 61

QY 117 RHLDKKRFHNIRGRTGRCMSSCRSSRTRETOL 151
      |||
DB 62 RHLDKKRFHNIRGRTGRCMSSCRSSRTRETOL 96

RESULT 12
US-08-860-165-14
; Sequence 14, Application US/08860165A
; Patent No. 6004557
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 17227/130
; CURRENT APPLICATION NUMBER: US/08/860,165A
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
; EARLIER APPLICATION NUMBER: AU PN0157
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Gene Fusion
US-08-860-165-14

Query Match          57.2%; Score 487; DB 3; Length 172;
Best Local Similarity 93.5%; Pred. No. 2e-44;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDDPERPRKLPQLCTELQTTIHDIILECYCKQOLLREYVDFAFRDLCIYVRDGNPY 60
      |||
DB 77 MFQDDPERPRKLPQLCTELQTTIHDIILECYCKQOLLREYVDFAFRDLCIYVRDGNPY 136

QY 61 AVCDCKLKFKYSKYSEYRHVCYSLYGTTLLEQOYN 93
      |||
DB 137 AVCDCKLKFKYSKYSEYRHVCYSLYGTTLRSHHH 169

RESULT 13
US-09-359-382-14
; Sequence 14, Application US/09359382
; Patent No. 6306397
; GENERAL INFORMATION:
; APPLICANT: EDWARDS, Stirling John
; APPLICANT: COX, John Cooper
; APPLICANT: WEBB, Elizabeth Ann
; APPLICANT: FRAZER, Ian
; TITLE OF INVENTION: VARIANTS OF HUMAN PAPILLOMA VIRUS ANTIGENS
; FILE REFERENCE: 017227/0148
; CURRENT APPLICATION NUMBER: US/09/359,382
; CURRENT FILING DATE: 1999-07-23
; EARLIER APPLICATION NUMBER: US 08/860,165
; EARLIER FILING DATE: 1997-09-22
; EARLIER APPLICATION NUMBER: PCT/AU95/00868
; EARLIER FILING DATE: 1995-12-20
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; EARLIER APPLICATION NUMBER: AU PN0157/94
; EARLIER FILING DATE: 1994-12-20
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent Ver. 2.0
; SEQ ID NO 14
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Human papillomavirus type 16
US-09-359-382-14

Query Match          57.2%; Score 487; DB 4; Length 172;
Best Local Similarity 93.5%; Pred. No. 2e-44;
Matches 87; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 MFQDDPERPRKLPQLCTELQTTIHDIILECYCKQOLLREYVDFAFRDLCIYVRDGNPY 60
      |||
DB 77 MFQDDPERPRKLPQLCTELQTTIHDIILECYCKQOLLREYVDFAFRDLCIYVRDGNPY 136

QY 61 AVCDCKLKFKYSKYSEYRHVCYSLYGTTLLEQOYN 93
      |||
DB 137 AVCDCKLKFKYSKYSEYRHVCYSLYGTTLRSHHH 169

RESULT 14
US-08-117-083-10
; Sequence 10, Application US/08117083
; Patent No. 5719054
; GENERAL INFORMATION:
; APPLICANT: Bourisnell, Michael E.
; APPLICANT: Ingalls, Stephen C.
; APPLICANT: Munro, Alan J.
; TITLE OF INVENTION: Recombinant Virus Vectors Encoding Human
; TITLE OF INVENTION: Papilloma Virus Proteins
; NUMBER OF SEQUENCES: 70
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Walter H. Dreger
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/117,083
; FILING DATE: 10-SEP-1993
; CLASSIFICATION: A35
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-58783
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-386-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 182 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..182
; OTHER INFORMATION: /note="Xaa refers to stop codon in
; OTHER INFORMATION: the open reading frame."
US-08-117-083-10

Query Match          56.3%; Score 479; DB 1; Length 182;
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Best Local Similarity 62.28; Pred. NO. 1.5e-43;  
Matches 97; Conservative 5; Mismatches 8; Indels 46; Gaps 4.

Search completed: December 13, 2002, 08:45:20  
Job time : 22.3067 secs

```
OY      1 MFQDQERPRKLPQLCTELQTTHIDIILECYCKQQLLRREYVDAFRDLCLIVADGNPY   60
        |||||||
Db       9 MFQDQERPRKLPQLCTELQTTHIDIILECYCKQQLLRREYVDAFRDLCLII----- 61
```

```

QY      61  A V C D K L F S K Y S E F R H Y C S L Y G T L L E Q Y K N P L C D L L I R C I N C Q K P L C P E E K Q R H L D 120
          |||||
Db      62  -----S E F R H Y C Y S L Y G T L L E Q Y -----E E K Q R H L D 88

```

```

QY      121 KKQRFHNIRGRWTC-----RCMSCCASSSTRRETQOL 151
          |||||
          ||: |
          ||: ||
Db      89 KKQRFHNIRGRWSCMEIHLHCMNICYIC-NQQRQVQL 123

```

RESULT 15  
US-08-247-904B-10

```

;
; GENERAL INFORMATION:
;
; APPLICANT: Rolfe, Mark
;
; APPLICANT: Eckstein, Jens W.

```

```

; TITLE OF INVENTION: Human Ubiquitin Conjugating Enzyme
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
;

```

STREET: One Post Office Square  
CITY: Boston  
STATE: MA

Query Match	Score 469.5:	DB 2.	length 158;
Best Local Similarity	55.1%:	Pred. No. 1.3e-42:	
Matches 87, Conservative 2%:	Mismatches 41;	Indels 5;	Gaps 1.

```

QY      2 FQDPPERPKRLQCLTELTQTTIHIIILECYCKQQLIRREYVDFAFRDLCTIVYRGKNPYA 61
      1: 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
DB      4 FEDPFRRRPYKLPDLCTELTNLSLOIIEITCYCKVTELTVEFEAFKDFVYRDSIPHA 63

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```

OY      62 VCDKCLFKFSYSEYRHHYCSLYGTTLEEQYNKPLCDLLIRCINQKPLCPPEEKQRHLD 121
      | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      64 ACHKCIDFYSRIRELRHHYSDSYVGDTEKLTNGLYNLLIRCLRQKPLPAEKLRLHNE 123

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```

QY      122 KQRFHNIRGWTGRCMSCCRSR-----TRREQL 151
        1:||||| : :| ||| :| |||||
Db      124 KRRFHNIRAGHYRGQCHSCSNARQLERLQRRREQL 158

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```
QY      122 KQRFHNIRGWTGRCMSCBSSR-----TRETQL 151
      1:||||| 1:1:1 ||| 1: |||||:
Db      124 KRRFHNIRGQCHSCCNARQERLQRRRETQV 158
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ID AAY02633 standard; Protein: 371 AA.  
 XX AAY02633;  
 XX  
 XX  
 XX 22-JUN-1999 (first entry)  
 DT  
 XX  
 XX Prot.D1/3-E6-E7-His/HPV16 protein.  
 DE  
 XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;  
 KM tumour; lesion; benign; malignant; virus; infection.  
 XX  
 XX OS Chimeric - Human papillomavirus.  
 OS Chimeric - Haemophilus influenzae.  
 XX  
 XX WO910375-A2.  
 PN  
 XX 04-MAR-1999.  
 PD  
 XX 17-AUG-1998; 98WO-EP05285.  
 PF  
 XX 22-AUG-1997; 97GB-0017953.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Bencheikh A;  
 PI  
 XX WPI: 1999-190587/16.  
 DR N-PSDB; AAX29782.  
 DR  
 XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions  
 CC  
 XX PS Disclosure; Fig 6; 95pp; English.  
 XX  
 XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
 CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Haemophilus influenzae B  
 CC protein D. The sequence also contains a histidine tag at the C-terminus  
 CC of the encoded protein. The protein can be used in a vaccine, for  
 CC immuno-therapeutically treating HPV induced tumour lesions (benign or  
 CC malignant) and preventing HPV viral infection.  
 CC  
 XX SQ Sequence 371 AA;  
 Query Match 99.1%; Score 843; DB 20; Length 371;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 60  
 DB 114 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 173  
 QY 61 AVCDKCLKFYSKYSEYRHGYSLVGTLEDOYKNPLCDLIRICINCKPKLPCEKORHLD 120  
 DB 174 AVCDKCLKFYSKYSEYRHGYSLVGTLEDOYKNPLCDLIRICINCKPKLPCEKORHLD 233  
 QY 121 KKQRFHNIRGWTGRMCMSCCRSSRTRETOL 151  
 DB 234 KKQRFHNIRGWTGRMCMSCCRSSRTRETOL 264

RESULT 15  
 AAY25381  
 ID AAY25381 standard; Protein: 390 AA.  
 XX AAY25381;  
 XX  
 XX  
 XX 06-SEP-1999 (first entry)  
 DT  
 XX  
 XX HPV fusion protein CLYTA-E6E7-His/HPV16.  
 DE  
 XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KW

KW Immunological fusion partner; Cpg oligonucleotide; immune response;  
 KM HPV antigen; prevention; treatment.  
 XX  
 XX Synthetic.  
 OS Human papillomavirus.  
 OS  
 XX WO933868-A2.  
 PN  
 XX 08-JUL-1999.  
 PD  
 XX 18-DEC-1998; 98WO-EP08563.  
 PF  
 XX 24-DEC-1997; 97GB-0027262.  
 PR  
 XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 PA  
 XX Dalemans WLJ, Gerard CMG;  
 PI  
 XX WPI: 1999-405485/34.  
 DR N-PSDB; AAX78797.  
 DR  
 XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV  
 CC  
 XX PS Example VII; Page 55-56; 62pp; English.  
 XX  
 XX AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory Cpg  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used  
 CC for preventing or treating HPV induced tumours.  
 CC  
 XX SQ Sequence 390 AA;  
 Query Match 99.1%; Score 843; DB 20; Length 390;  
 Best Local Similarity 99.3%; Pred. No. 2.9e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 60  
 DB 133 MFODPQERPRKLPOLCTELQTTIHDIILECYCKQQLLRREVDFAFRDLCIYRDGNPY 192  
 QY 61 AVCDKCLKFYSKYSEYRHGYSLVGTLEDOYKNPLCDLIRICINCKPKLPCEKORHLD 120  
 DB 193 AVCDKCLKFYSKYSEYRHGYSLVGTLEDOYKNPLCDLIRICINCKPKLPCEKORHLD 252  
 QY 121 KKQRFHNIRGWTGRMCMSCCRSSRTRETOL 151  
 DB 253 KKQRFHNIRGWTGRMCMSCCRSSRTRETOL 283

Search completed: December 13, 2002, 08:38:15  
 Job time : 60.362 secs

Query Match 99.1%; Score 843; DB 20; Length 292;  
 Best Local Similarity 99.3%; Pred. No. 2.1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 133 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 192

QY 61 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 193 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 252

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 253 KQRFHNRGRWTRGCMSCCRSSRTRETQL 283

RESULT 12  
 AAY02635  
 ID AAY02635 standard; Protein: 292 AA.  
 AC AAY02635;  
 XX  
 DT 22-JUN-1999 (first entry)  
 XX  
 DE CLYTA-E6-His protein.  
 XX  
 KM Chimeric; E6; E7; fusion protein; CLYTA; vaccine; immunotherapy;  
 XX tumour; lesion; benign; malignant; virus; infection.  
 XX  
 OS Chimeric - Human papillomavirus.  
 OS Chimeric - Streptococcus pneumoniae.  
 XX  
 PN WO910375-A2.  
 XX  
 PD 04-MAR-1999.  
 XX  
 PF 17-AUG-1998; 98WO-EP05285.  
 XX  
 PR 22-AUG-1997; 97GB-0017953.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;  
 PI Lombardo-Benchelkh A;  
 XX  
 DR WPI; 1999-190587/16.  
 XX  
 DR N-PSDB; AAX29784.  
 XX  
 PT Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for  
 PT treatment or prophylaxis of HPV induced lesions  
 XX  
 PS Disclosure; Fig 10; 95pp; English.  
 XX  
 CC This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion  
 CC protein from Human papillomavirus (HPV) linked to an immunological fusion  
 CC partner, in this case, a fragment of the Streptococcus pneumoniae CLYTA  
 CC protein of the encoded protein. The protein can be used in a vaccine,  
 CC for immuno-therapeutically treating HPV induced tumour lesions (benign  
 CC or malignant) and preventing HPV viral infection.  
 CC  
 XX  
 SQ Sequence 292 AA;

Query Match 99.1%; Score 843; DB 20; Length 292;  
 Best Local Similarity 99.3%; Pred. No. 2.1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 133 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 192

QY 61 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 193 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 252

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 253 KQRFHNRGRWTRGCMSCCRSSRTRETQL 283

RESULT 13  
 AAY25377  
 ID AAY25377 standard; Protein: 371 AA.  
 AC AAY25377;  
 XX  
 DT 06-SEP-1999 (first entry)  
 XX  
 DE HPV fusion protein DI/3-E6E7-His/HPV16.  
 XX  
 KM Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;  
 KM immunological fusion partner; CPG oligonucleotide; immune response;  
 KM HPV antigen; prevention; treatment.  
 XX  
 OS Synthetic.  
 OS Human papillomavirus.  
 XX  
 PN WO933868-A2.  
 XX  
 PD 08-JUL-1999.  
 XX  
 PF 18-DEC-1998; 98WO-EP08563.  
 XX  
 PR 24-DEC-1997; 97GB-0027262.  
 XX  
 PA (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
 XX  
 PI Dalemans WLJ, Gerard CMG;  
 PI  
 XX  
 DR WPI; 1999-405485/34.  
 XX  
 DR N-PSDB; AAX78793.  
 XX  
 PT Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to  
 PT induce immune response to HPV  
 XX  
 PS Example III; Page 50; 62pp; English.  
 XX  
 CC AAX78791-X78801 represent nucleic acid sequences which encode novel  
 CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from  
 CC HPV (represented in AAY25375-Y25386). These constructs are optionally  
 CC linked to an immunological fusion partner and an immunomodulatory CPG  
 CC oligonucleotide. The products of the invention can be used to induce an  
 CC immune response in a patient to an HPV antigen. They can also be used  
 CC for preventing or treating HPV induced tumours.  
 CC  
 XX  
 SQ Sequence 371 AA;

Query Match 99.1%; Score 843; DB 20; Length 371;  
 Best Local Similarity 99.3%; Pred. No. 2.7e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 60  
 |||||||  
 DB 114 MFQDPQRPRLPOLCTELQTTTHDITILECVYCKQQLLRREYVDFAFRDLCTIYRDGNPY 173

QY 61 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 120  
 |||||||  
 DB 174 AVCDKCLKFKFSKSEYRHVCYSXGTTLEQYNNKPLCDLLIRINCOKPLCPBEKORHLD 233

QY 121 KQRFHNRGRWTRGCMSCCRSSRTRETQL 151  
 |||||||  
 DB 234 KQRFHNRGRWTRGCMSCCRSSRTRETQL 264

RESULT 14  
 AAY02633

```

DR WPI; 1999-405485/34.
DR N-PSDB; AAX78792.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV
PS Example II; Page 48-49; 62pp; English.
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used
CC for preventing or treating HPV induced tumours.
XX
XX Sequence 273 AA;
SQ
Query Match 99.1%; Score 843; DB 20; Length 273;
Best Local Similarity 99.3%; Pred. No. 1.9e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MFODPQRPRLPOLCTELQTTIHIDILCEVCCKQQLLRREVDFAFRLDCIYRDGNPY 60
DB 114 MFODPQRPRLPOLCTELQTTIHIDILCEVCCKQQLLRREVDFAFRLDCIYRDGNPY 173
QY 61 AVCDKCLKFSKYSEYRHYCSLYGTTLEOQYNKPLCDLLIRINCQKPLCPBEKQRLHD 120
DB 174 AVCDKCLKFSKYSEYRHYCSLYGTTLEOQYNKPLCDLLIRINCQKPLCPBEKQRLHD 233
QY 121 KKQRFHNIIRGWTGRMCCSCRSSSTRRETOL 151
DB 234 KKQRFHNIIRGWTGRMCCSCRSSSTRRETOL 264
DE
RESULT 10
AAY02632
ID AAY02632 standard; Protein: 273 AA.
XX
XX AAY02632;
AC
XX 22-JUN-1999 (first entry)
DT
XX
XX Prot.D1/3-E6-His/HPV16 protein.
DE
XX Chimeric; E6; E7; fusion protein; protein D; vaccine; immunotherapy;
KW tumour; lesion; benign; malignant; virus; infection.
XX
XX Chimeric - Human papillomavirus.
OS
XX Chimeric - Haemophilus influenzae.
XX
XX WO9910375-A2.
PN
XX 04-MAR-1999.
PD
XX 17-AUG-1998; 98WO-EP05285.
PF
XX 22-AUG-1997; 97GB-0017953.
PR
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Bruck C, Cabezon Silva T, Delisse AEF, Gerard CMG;
PI Lombardo-Bencheikh A;
PS
XX WPI; 1999-190587/16.
DR N-PSDB; AAX29781.
XX
XX Human Papilloma Virus (HPV) fusion proteins - useful in vaccines for
PT treatment or prophylaxis of HPV induced lesions
XX
XX Disclosure; Fig 3; 95pp; English.
XX
XX This sequence represents a chimeric E6 or E7 protein or E6/E7 fusion
CC

```

```

CC protein from Human papillomavirus (HPV) linked to an immunological fusion
CC partner, in this case, a fragment of the Haemophilus influenzae B
CC protein D. The sequence also contains a histidine tag at the C-terminus
CC of the encoded protein. The protein can be used in a vaccine, for
CC immuno-therapeutically treating HPV induced tumour lesions (benign or
CC malignant) and preventing HPV viral infection.
XX
XX Sequence 273 AA;
SQ
Query Match 99.1%; Score 843; DB 20; Length 273;
Best Local Similarity 99.3%; Pred. No. 1.9e-82;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MFODPQRPRLPOLCTELQTTIHIDILCEVCCKQQLLRREVDFAFRLDCIYRDGNPY 60
DB 114 MFODPQRPRLPOLCTELQTTIHIDILCEVCCKQQLLRREVDFAFRLDCIYRDGNPY 173
QY 61 AVCDKCLKFSKYSEYRHYCSLYGTTLEOQYNKPLCDLLIRINCQKPLCPBEKQRLHD 120
DB 174 AVCDKCLKFSKYSEYRHYCSLYGTTLEOQYNKPLCDLLIRINCQKPLCPBEKQRLHD 233
QY 121 KKQRFHNIIRGWTGRMCCSCRSSSTRRETOL 151
DB 234 KKQRFHNIIRGWTGRMCCSCRSSSTRRETOL 264
DE
RESULT 11
AAY25379
ID AAY25379 standard; Protein: 292 AA.
XX
XX AAY25379;
AC
XX 06-SEP-1999 (first entry)
DT
XX
XX HPV fusion protein CLYTA-E6-His/HPV16.
DE
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
KW immunological fusion partner; CpG oligonucleotide; immune response;
KW HPV antigen; prevention; treatment.
XX
XX Synthetic.
OS
XX Human papillomavirus.
XX
XX WO9933868-A2.
PN
XX 08-JUL-1999.
PD
XX 18-DEC-1998; 98WO-EP08563.
PF
XX 24-DEC-1997; 97GB-0027262.
PR
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
PA
XX Dalemans WLJ, Gerard CMG;
PI
XX WPI; 1999-405485/34.
DR N-PSDB; AAX78795.
XX
XX Composition comprising an E6, E7 or E6/E7 fusion protein from HPV to
PT induce immune response to HPV
PS
XX Example VI; Page 52-53; 62pp; English.
XX
XX AAX78791-X78801 represent nucleic acid sequences which encode novel
CC constructs comprising an E6 or E7 protein or E6/E7 fusion protein from
CC HPV (represented in AAY25375-Y25386). These constructs are optionally
CC linked to an immunological fusion partner and an immunomodulatory CpG
CC oligonucleotide. The products of the invention can be used to induce an
CC immune response in a patient to an HPV antigen. They can also be used
CC for preventing or treating HPV induced tumours.
XX
XX Sequence 292 AA;
SQ

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```
XX 14-MAR-1991: 91GB-0005383.
XX
XX (IMMU ) IMMUNOLOGY LTD.
XX
XX Boursnell MEG, Inglis SC, Munro AJ;
XX
XX WPI: 1992-349219/42.
XX
XX N-PSDB; AAQ29389.
XX
XX Recombinant virus vectors encoding human papillomavirus proteins
XX - for treating and vaccinating against HPV infections and
XX conditions caused by them, such as cervical cancer
XX
XX
XX Disclosure: Fig 1a; 83pp; English.
XX
XX The fragment of DNA contg. the HPV-16 E6/E7 coding region was
XX prep'd. by PCR from plasmid pBR322/HPV16 (Durst et al., PNAS, 80:
XX 3812 (1983)) using oligonucleotides S05 and S06. The prod. of the
XX third reading frame is the HPV-16 E6 protein whereas the second
XX reading frame encodes HPV-16 E7. The E6 and E7 ORFs are fused
XX together to form a single continuous ORF via site directed mutagenesis
XX and the immortalising potential of E7 is removed by altering two key
XX codons of the HPV E7 sequence. The single ORF of HPV-16 E6/E7 may be
XX inserted into vaccinia virus DNA at neutral sites (pref. by inserting
XX two sets of the DNA in opposite orientations to overcome the problem
XX of intertypic recombination) to make a recombinant virus vector for
XX use immunotherapeutically to activate cells of the immune system
XX against HPV. See also AAR27723-43.
XX
XX
XX Sequence 263 AA:
XX
XX Query Match 99.1%; Score 843; DB 13; Length 263;
XX Best Local Similarity 99.3%; Pred. No. 1.8e-82;
XX Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 60
XX |
XX DB 9 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 68
XX
XX QY 61 AVCDKCLKFYSKYSEYRHYCSLYGTTLEQYKPKLDLIRINCQKPLCPBEKQRHLD 120
XX |
XX DB 69 AVCDKCLKFYSKYSEYRHYCSLYGTTLEQYKPKLDLIRINCQKPLCPBEKQRHLD 128
XX
XX QY 121 KQRFNINIRGRTGRCMSCCRSSRTRETQL 151
XX |
XX DB 129 KQRFNINIRGRTGRCMSCCRSSRTRETQL 159
XX
XX
XX RESULT 8
XX AAR97561
XX ID AAR97561 standard; Protein; 266 AA.
XX
XX AC AAR97561;
XX
XX 11-JAN-1997 (first entry)
XX
XX Human papilloma virus E6/E7 protein variant.
XX
XX Human papilloma virus; E6; E7; deletion mutant; HPV;
XX immune response; humoral immune response; cellular immune response;
XX vaccine.
XX
XX Human papilloma virus.
XX
XX WO9619496-A1.
XX
XX 27-JUN-1996.
XX
XX 20-DEC-1995; 95WO-AU00868.
XX
XX 20-DEC-1994; 94AU-0000157.
XX
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PA (CSLC-) CSL LTD.
PA (UYQU ) UNIV QUEENSLAND.
XX
XX Cox J, Edwards SJ, Frazer I, Webb EA;
XX
XX WPI: 1996-309518/31.
XX
XX N-PSDB; AAT31833.
XX
XX Vaccine variants of human papilloma virus antigens - contain
XX variants of E6 and/or E7 protein, pref. deletion mutants, and are
XX used to treat or prevent HPV infection
XX
XX Example 1; Page 15-16; 37pp; English.
XX
XX A variant of the human papilloma virus (HPV) E6 or E7 protein which
XX elicits a humoral and/or cellular immune response against HPV can be
XX used in vaccines against HPV or to treat HPV infection. The variant
XX is preferably a deletion mutant comprising at least half, and
XX preferably two-thirds of full length E6 or E7 protein starting from
XX the N- or C-terminal, or is a full length E6 moiety fused to a full
XX length E7 moiety. The variant optionally has a linkage moiety and a
XX foreign protein or peptide which facilitates the purification of,
XX and enhances the immunogenicity of, the fusion protein. This
XX sequence is a full length E6/E7 fusion protein.
XX
XX
XX Sequence 266 AA:
XX
XX Query Match 99.1%; Score 843; DB 17; Length 266;
XX Best Local Similarity 99.3%; Pred. No. 1.8e-82;
XX Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 60
XX |
XX DB 8 MFQDPQERPRKLPQLCTELQTTIHDIILECVYCKQQLRREYVDFAFRDLCTIYRDGNPY 67
XX
XX QY 61 AVCDKCLKFYSKYSEYRHYCSLYGTTLEQYKPKLDLIRINCQKPLCPBEKQRHLD 120
XX |
XX DB 68 AVCDKCLKFYSKYSEYRHYCSLYGTTLEQYKPKLDLIRINCQKPLCPBEKQRHLD 127
XX
XX QY 121 KQRFNINIRGRTGRCMSCCRSSRTRETQL 151
XX |
XX DB 128 KQRFNINIRGRTGRCMSCCRSSRTRETQL 158
XX
XX
XX RESULT 9
XX AAY25376
XX ID AAY25376 standard; Protein; 273 AA.
XX
XX AC AAY25376;
XX
XX 06-SEP-1999 (first entry)
XX
XX HPV fusion protein DI/3-E6-His/HPV16.
XX
XX Fusion protein; E6 protein; E7 protein; E6/E7; immunomodulator; tumour;
XX immunological fusion partner; CPG oligonucleotide; immune response;
XX HPV antigen; prevention; treatment.
XX
XX Synthetic.
XX
XX Human papillomavirus.
XX
XX WO9933868-A2.
XX
XX 08-JUL-1999.
XX
XX 18-DEC-1998; 98WO-EP08563.
XX
XX 24-DEC-1997; 97GB-0027262.
XX
XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.
XX
XX Dalemans WLJ, Gerard CMG;
XX
```



PF 28-SEP-1993; 93US-0127906.  
 XX  
 PR 30-SEP-1994; 94US-0316239.  
 PR 28-SEP-1993; 93US-0127906.  
 XX  
 PA (UYNE-) UNIV NEW MEXICO STATE.  
 XX  
 PI Parmenter CA, Wheeler CW;  
 XX  
 DR WPI: 1997-525714/48.  
 DR N-PSDB; AAT94723.  
 XX  
 PT Evaluating risk of cervical dysplasia or cervical cancer - by  
 PT detecting variant form of human papilloma virus 16  
 XX  
 PS Claim 7; Column 23-24; 33pp; English.  
 XX  
 CC Methods have been developed for distinguishing a subset of human  
 CC papilloma virus (HPV) that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The methods involve:  
 CC (1) preparing a cervical sample to expose any HPV-16 E6 gene in the  
 CC sample and determining if the base at position 350 of the E6 gene  
 CC (see AAT94723 and AAT94724 for comparison) is T or G, where the presence  
 CC of G at position 350 is associated with an increased risk of developing  
 CC cervical dysplasia or cervical cancer; and (2) preparing a cervical  
 CC sample to expose any HPV-16 E6 protein in the sample and determining  
 CC if the amino acid at position 83 of the protein (see position 90 in  
 CC AAM3741 and AAM3742 for comparison) is Val or Leu, where the presence  
 CC of Val at position 83 that is associated with an increased risk of  
 CC developing cervical dysplasia or cervical cancer. The present sequence  
 CC represents the reference protein sequence for HPV-16 E6. The 350G  
 CC variant correlates well with Pap scores: 350T:350G ratios among 45  
 CC HPV16 samples were 10:4 for negative Pap scores; 4:2 for CIN I, 1:6 for  
 CC CIN II; 2:9 for CIN III; 0:3 for cancer.  
 XX  
 SQ Sequence 162 AA:  
 Query Match 99.1%; Score 843; DB 18; Length 162;  
 Best Local Similarity 99.3%; Pred. No. 1e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFDDPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCIYRGDNPY 60  
 DB 8 MFDDPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCIYRGDNPY 67  
 QY 61 AVCDKCLKFYSKSEYRHYCYSLYGTLLLEQYNNKPLCDLLIRICINCKPLCPEKORHLD 120  
 DB 68 AVCDKCLKFYSKSEYRHYCYSLYGTLLLEQYNNKPLCDLLIRICINCKPLCPEKORHLD 127  
 QY 121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151  
 DB 128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158  
 RESULT 6  
 AAR63865  
 ID AAR63865 standard; protein; 188 AA.  
 XX  
 AC AAR63865;  
 XX  
 DT 28-JUN-1995 (first entry)  
 XX  
 DE HPV16 E6/E7 proteins.  
 XX  
 KW HPV, HPV16; E6 protein; E7 protein; diagnosis; cervical dysplasia;  
 KW cervix cancer.  
 XX  
 OS Human papillomavirus strain 16.  
 XX  
 FH Key Location/Qualifiers  
 FT Protein 1..158  
 FT /label= E6-protein  
 FT Protein 159..188

FT /label= E7-protein  
 XX  
 PN WO9426934-A.  
 XX  
 PD 24-NOV-1994.  
 XX  
 PF 06-MAY-1994; 94WO-US05085.  
 XX  
 PR 06-MAY-1993; 93US-0058920.  
 XX  
 PA (BAXT ) BAXTER DIAGNOSTICS INC.  
 XX  
 PI Brown JT;  
 XX  
 DR WPI: 1995-006821/01.  
 DR P-PSDB; AAO75470.  
 XX  
 PT Human papilloma virus detection assay - by amplification using  
 PT self sustained sequence replication and hybridisation with a  
 PT detector probe  
 XX  
 PS Disclosure; Page 24-26; 79pp; English.  
 XX  
 CC The sequences of the E6 and E7 polypeptide-encoding regions of human  
 CC papillomavirus (HPV) 16 and 18 are given in AAO75470-71 and the  
 CC encoded proteins in AAR63865-66, respectively. Probes and primers  
 CC based on these sequences were used for HPV infection diagnosis;  
 CC expression of E6 and E7 is diagnostic for cervical cancer or pre-  
 CC malignant states.  
 XX  
 SQ Sequence 188 AA:  
 Query Match 99.1%; Score 843; DB 16; Length 188;  
 Best Local Similarity 99.3%; Pred. No. 1.2e-82;  
 Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFDDPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCIYRGDNPY 60  
 DB 8 MFDDPOERPRKLPOLCTELQTTIHDIIECYCKQQLRREYVDFAFRDLCIYRGDNPY 67  
 QY 61 AVCDKCLKFYSKSEYRHYCYSLYGTLLLEQYNNKPLCDLLIRICINCKPLCPEKORHLD 120  
 DB 68 AVCDKCLKFYSKSEYRHYCYSLYGTLLLEQYNNKPLCDLLIRICINCKPLCPEKORHLD 127  
 QY 121 KROFHNIRGRMTGRMCCRSSSTRRETOL 151  
 DB 128 KROFHNIRGRMTGRMCCRSSSTRRETOL 158  
 RESULT 7  
 AAR77725  
 ID AAR77725 standard; protein; 263 AA.  
 XX  
 AC AAR77725;  
 XX  
 DT 09-MAR-1993 (first entry)  
 XX  
 DE HPV 16 E6 protein fragment.  
 XX  
 KW Virus vector; vaccinia virus; papillomavirus; HPV; human;  
 KW amplification; immunotherapeutic.  
 XX  
 OS Human papillomavirus 16.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..159  
 FT /note= "HPV-16 E6 protein"  
 XX  
 PN WO9216636-A.  
 XX  
 PD 01-OCT-1992.  
 XX  
 PF 10-MAR-1992; 92WO-GB00424.

PI Bernard H, Tan YJ, Beerheide W, Ting AE, Sim MM;  
 XX WPI: 2000-256917/22.  
 PT Polysulfide and dithionodisulfide agents, useful for the treatment or  
 XX prophylaxis of diseases caused by mammalian papillomavirus, are  
 PT disruptors of a chelated metal cation domain in an MPV gene encoded  
 PS protein.  
 XX Disclosure: Fig 1; 78pp; English.  
 CC The present invention describes an agent used in the treatment or  
 CC prophylaxis of a disease caused or exacerbated by MPV (mammalian  
 CC papillomavirus) comprising a compound capable of reducing, inhibiting  
 CC or otherwise decreasing the activity of a protein encoded by an MPV  
 CC gene by facilitating disruption of a chelated metal cation domain  
 CC present in the protein. An agent of the present invention can be used  
 CC to treat cervical cancer or its HPV associated precursor lesions or  
 CC other HPV associated cancers and/or warts. The present sequence  
 CC represents a human papillomavirus E6 protein containing two zinc  
 CC finger motifs, as given in the exemplification of the present  
 CC invention.  
 XX  
 SQ Sequence 158 AA;  
 Query Match 99.1%; Score 843; DB 21; Length 158;  
 Best Local Similarity 99.3%; Pred. No. 1e-82;  
 Matches 150: Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 60  
 DB 8 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 67  
 QY 61 AVCDCKLKFSKYSSEYRHCYSLYGTTLEQYKNPKCDLLINCINQKRLCEPEKORHD 120  
 DB 68 AVCDCKLKFSKYSSEYRHCYSLYGTTLEQYKNPKCDLLINCINQKRLCEPEKORHD 127  
 QY 121 KKQRFHINIRGWTGRCMSCCRSSRTTRETOL 151  
 DB 128 KKQRFHINIRGWTGRCMSCCRSSRTTRETOL 158  
 RESULT 4  
 AAB98420  
 ID AAB98420 standard; Protein: 158 AA.  
 XX  
 AC AAB98420;  
 DT 22-AUG-2001 (first entry)  
 XX  
 DE Human papillomavirus protein HPV16 E6.  
 XX  
 KW Human papillomavirus; human leukocyte antigen; HLA; immune response;  
 KW HPV; epitope; T cell; identification; vaccine; infection; genital wart;  
 KW neoplastic growth; antiviral.  
 XX  
 OS Human papillomavirus.  
 XX  
 PN WO200141799-A1.  
 XX  
 PD 14-JUN-2001.  
 XX  
 PF 11-DEC-2000; 2000WO-US33549.  
 XX  
 PR 10-DEC-1999; 99US-0172705.  
 PR 15-AUG-2000; 2000US-0641528.  
 XX  
 PA (EPIM-) EPIMMUNE INC.  
 XX  
 PI Sette A, Sidney J, Southwood S, Chesnut R, Celis E, Grey HM;  
 XX WPI: 2001-381497/40.  
 XX

PT An isolated human papilloma virus (HPV) epitope, useful in vaccines for  
 PT treating HPV infections -  
 XX  
 PS Disclosure: Page 20-21; 756pp; English.  
 CC The present invention describes an isolated prepared human papillomavirus  
 CC (HPV) epitope (I). (I) has antiviral activity, and can be used in  
 CC vaccine production. Peptides and corresponding nucleic acid compositions  
 CC from the present invention are useful for stimulating an immune response  
 CC to HPV by stimulating the production of CTL or HTL responses,  
 CC specifically in the treatment or prophylaxis of HPV infection, in persons  
 CC who have not manifested symptoms e.g. genital warts or neoplastic growth.  
 CC The peptides can also be used in a tetramer staining assay to assess  
 CC peripheral blood mononuclear cells for the presence of antigen-specific  
 CC CTLs following exposure to a pathogen or immunogen, and as reagents to  
 CC evaluate immune recall responses or evaluate the efficacy of a vaccine.  
 CC The vaccine compositions are useful for removing warts or treating HPV  
 CC infections. The epitopes for inclusion in an epitope-base vaccine may  
 CC be selected from conserved regions of viral or tumour-associated  
 CC antigens, which reduces the likelihood of escape mutants, also  
 CC immunosuppressive epitopes that may be present in whole antigens can be  
 CC avoided with the use of epitope-base vaccines. An additional advantage  
 CC is the ability to combine selected epitopes (CTL and HTL) and to modify  
 CC the composition of the epitopes achieving enhanced immunogenicity, the  
 CC major benefit of the vaccine is that is safe and efficacious. AAB98391  
 CC to AAB98477 represent polypeptide sequences used in the exemplification  
 CC of the present invention.  
 XX  
 SQ Sequence 158 AA;  
 Query Match 99.1%; Score 843; DB 22; Length 158;  
 Best Local Similarity 99.3%; Pred. No. 1e-82;  
 Matches 150: Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 60  
 DB 8 MFQDPQERPRKLPQLCTELQTTIHDIIECVYCKQQLRREYDFAFRLDCTIVYRDGNY 67  
 QY 61 AVCDCKLKFSKYSSEYRHCYSLYGTTLEQYKNPKCDLLINCINQKRLCEPEKORHD 120  
 DB 68 AVCDCKLKFSKYSSEYRHCYSLYGTTLEQYKNPKCDLLINCINQKRLCEPEKORHD 127  
 QY 121 KKQRFHINIRGWTGRCMSCCRSSRTTRETOL 151  
 DB 128 KKQRFHINIRGWTGRCMSCCRSSRTTRETOL 158  
 RESULT 5  
 AAW35741  
 ID AAW35741 standard; Protein: 162 AA.  
 XX  
 AC AAW35741;  
 DT 16-FEB-1998 (first entry)  
 XX  
 DE Human papillomavirus type 16 E6 protein.  
 XX  
 KW Complete genome; circular; human papillomavirus type 16; HPV16 E6;  
 KW cervical dysplasia; cervical cancer; cervical smear.  
 XX  
 OS Human papillomavirus type 16.  
 XX  
 PN  
 PD  
 PF  
 FT Key Location/Qualifiers  
 FT Misc-difference 90 /note= "Mutated to Val in the variant"  
 FT Misc-difference 159 /note= "End of protein sequence even though 3 amino  
 FT /note= "acid residues are given following on"  
 XX  
 XX US5679509-A.  
 XX  
 PN  
 PD 21-OCT-1997.  
 XX

XX Example 2: Fig 9; 73pp; English.

PS The present invention describes a polypeptide comprising a  
CC transcripional adaptor motif (TRAM) or a TRAM-interaction motif  
CC (TRIM) (I). (I) can be used for identifying compounds (II) comprising a  
CC polypeptide capable of disrupting an interaction between a TRAM sequence  
CC and/or a TRIM sequence. Polypeptides which bind to a TRAM sequence or a  
CC TRIM sequence are identified by incubating, the polypeptide with (I) and  
CC determining if the polypeptide interacts with (I). Compound (II) is  
CC useful for preparing a pharmaceutical composition and for disrupting an  
CC interaction between TRAM sequence and TRIM sequence in vitro, thereby  
CC inhibiting viral transcription or cell cycle progression in mammalian  
CC cells especially cancer cell. Compounds which disrupt interaction  
CC between TRIM/TRAM containing polypeptides can be used therapeutically to  
CC prevent or treat viral diseases and tumours. The polypeptides reduce  
CC susceptibility of cells to viral infection and regulate cell cycle  
CC including apoptosis and growth arrest and can be used to produce  
CC antibodies against the TRIM or TRAM sequences. HPV types associated  
CC with high risk or low risk of cervical cancer can be distinguished  
CC based on the ability of E6 polypeptides to bind to creb binding protein  
CC (CBP) TRAM sequence. The present sequence represents a HPV-16 E6 protein  
CC amino acid sequence from an example from the present invention.

XX Sequence 151 AA:

Query Match 100.0%; Score 851; DB 21; Length 151;  
Best Local Similarity 100.0%; Pred. No. 1.3e-83;  
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVYDFARDCIYRDGPNY 60

Db 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVYDFARDCIYRDGPNY 60

QY 61 AVCDKCLKFSKYSEYHYHCYSLXGTLLEQYNNPLCDLLIRINCQKPLCPBEKQRLD 120

Db 61 AVCDKCLKFSKYSEYHYHCYSLXGTLLEQYNNPLCDLLIRINCQKPLCPBEKQRLD 120

QY 121 KQRFHNIRGWTGRMCSRSSRTRETOL 151

Db 121 KQRFHNIRGWTGRMCSRSSRTRETOL 151

RESULT 2  
AAR22766  
ID AAR22766 standard; peptide; 158 AA.

XX AAR22766;

XX 21-SEP-1992 (first entry)

XX HPV E6 peptide.

XX Human; papillomavirus; immunogenic; cervical; warts; carcinoma;  
KW cancer.

XX Synthetic.

OS Homo sapiens.

XX W09205248-A.

XX 02-APR-1992.

XX 26-SEP-1991; 91WO-US07081.

XX 26-SEP-1990; 90US-0588384.

XX (BRIM ) BRISTOL-MYERS SQUIB.

XX Blake J, Chen L, Hellstrom I, Hellstrom K, Hu S L;

XX Thomas E K;

XX WPI; 1992-132119/16.

XX Immunogenic peptide(s) derived from E6 or E7 region of HPV16 -  
PT and recombinant cells encoding them, useful in treatment and  
PT prophylaxis of cervical warts or cancer resulting from HPV  
PT infection

XX Disclosure; Fig 7; 81pp; English.

CC The peptide is the sequence of the human papillomavirus HPV 16 E6  
CC nucleoprotein. Peptides corresponding to regions (pref, epitopic  
CC regions) of HPV 16 E6 were synthesised by standard Merrifield  
CC synthesis. Examples of such peptides are E6 1-20, 8-20, 119-134 or  
CC 148-158. Compositions contg. these peptides, antibodies against the  
CC peptides, or recombinant cells contg. the gene encoding the immuno-  
CC genic peptides may be utilised in methods for inhibiting and treating  
CC HPV infection and tumour initiation and progression e.g. in the  
CC prevention or retardation of cervical warts and cervical carcinoma  
CC resulting from HPV infection.  
CC See also AAR22767.

XX Sequence 158 AA:

Query Match 99.1%; Score 843; DB 13; Length 158;  
Best Local Similarity 99.3%; Pred. No. 1e-82;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVYDFARDCIYRDGPNY 60

Db 8 MFODPQERPRKLPQCTELQTTIHDIIECYCKQQLRREVYDFARDCIYRDGPNY 67

QY 61 AVCDKCLKFSKYSEYHYHCYSLXGTLLEQYNNPLCDLLIRINCQKPLCPBEKQRLD 120

Db 68 AVCDKCLKFSKYSEYHYHCYSLXGTLLEQYNNPLCDLLIRINCQKPLCPBEKQRLD 127

QY 121 KQRFHNIRGWTGRMCSRSSRTRETOL 151

Db 128 KQRFHNIRGWTGRMCSRSSRTRETOL 158

RESULT 3  
AA82462  
ID AA82462 standard; Protein; 158 AA.

XX AA82462;

XX 30-JUN-2000 (first entry)

XX Human papillomavirus E6 protein containing two zinc finger motifs.

XX Chelated zinc finger; therapeutic; treatment; prophylaxis; MPV;  
KW mammalian papillomavirus; antiviral; cytostatic; cervical cancer;  
XX lesion; wart.

XX Human papillomavirus.

OS Human papillomavirus.

XX Key Location/Qualifiers

FT Misc-difference 37..73

FT /note- "forms a zinc finger motif"

FT Misc-difference 110..146

FT /note- "forms a zinc finger motif"

XX W0200014063-A1.

XX 16-MAR-2000.

XX 03-SEP-1999; 99WO-AU00724.

XX 04-SEP-1998; 98AU-0005733.

XX 15-JUL-1999; 99AU-0001645.

XX (MOLE-) INST MOLECULAR & CELL BIOLOGY.

XX (HUGH/) HUGHES E J L.

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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:04 : Search time 58.362 Seconds  
(without alignments)  
344.760 Million cell updates/sec

Title: US-09-701-080c-18  
Perfect score: 851  
Sequence: 1 MFQDPEPRPKLPOLCTEHLQ.....WTGRCMSCCRSRTRETFQL 151

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 13350620 residues  
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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3: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1982.DAT:\*  
4: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1983.DAT:\*  
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6: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1985.DAT:\*  
7: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1986.DAT:\*  
8: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1987.DAT:\*  
9: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1988.DAT:\*  
10: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1989.DAT:\*  
11: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1990.DAT:\*  
12: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1991.DAT:\*  
13: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1992.DAT:\*  
14: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1993.DAT:\*  
15: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1994.DAT:\*  
16: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1995.DAT:\*  
17: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1996.DAT:\*  
18: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1997.DAT:\*  
19: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1998.DAT:\*  
20: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA1999.DAT:\*  
21: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA2000.DAT:\*  
22: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA2001.DAT:\*  
23: /SIDS2/gcgdata-a/geneseq/geneseqp-emb1/AA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851	100.0	151	21	AAV57808
2	843	99.1	158	13	AAV57808
3	843	99.1	158	21	AAV57808
4	843	99.1	158	22	AAV57808
5	843	99.1	162	18	AAV57808
6	843	99.1	162	16	AAV57808
7	843	99.1	263	13	AAV57808
8	843	99.1	266	17	AAV57808
9	843	99.1	273	20	AAV57808
10	843	99.1	273	20	AAV57808

11	843	99.1	292	20	AAV57808	HPV fusion protein
12	843	99.1	292	20	AAV57808	CLYRA-E6-His prote
13	843	99.1	371	20	AAV57808	HPV fusion protein
14	843	99.1	371	20	AAV57808	Prot.D1/3-E6-E7-H1
15	843	99.1	371	20	AAV57808	HPV fusion protein
16	843	99.1	371	20	AAV57808	CLYRA-E6E7-His pro
17	840	98.7	300	20	AAV57808	Human papillomavir
18	799.5	93.9	243	18	AAV57808	Papillomavirus E6/
19	594	69.8	149	14	AAV57808	HPV E6 region prod
20	538	63.2	149	22	AAV57808	Human papillomavir
21	534	62.7	149	22	AAV57808	Human papillomavir
22	487	57.2	172	17	AAV57808	Human papilloma v1
23	477	56.1	172	17	AAV57808	Human papilloma v1
24	469.5	55.2	158	16	AAV57808	HPV-18 E6 protein.
25	469.5	55.2	158	16	AAV57808	HPV18 E6/E7 protel
26	469.5	55.2	158	20	AAV57808	HPV-18 E6 protein
27	469.5	55.2	158	21	AAV57808	HPV-18 E6 protein.
28	469.5	55.2	158	22	AAV57808	Human papillomavir
29	469.5	55.2	278	20	AAV57808	HPV fusion protein
30	469.5	55.2	278	20	AAV57808	Prot.D1/3-E6-His/H
31	469.5	55.2	278	20	AAV57808	HPV fusion protein
32	469.5	55.2	383	20	AAV57808	Prot.D1/3-E6-E7-H1
33	469.5	55.2	383	20	AAV57808	Human papillomavir
34	460.5	54.1	158	22	AAV57808	Human papillomavir
35	441.5	51.9	155	22	AAV57808	Human papillomavir
36	332	38.9	236	22	AAV57808	Polyepitope polype
37	331	39.0	117	22	AAV57808	Polyepitope polype
38	321	37.7	150	22	AAV57808	Human papillomavir
39	320	37.6	150	22	AAV57808	Human papillomavir
40	320	37.6	368	18	AAV57808	Human papillomavir
41	320	37.6	375	18	AAV57808	Human papillomavir
42	320	37.6	465	18	AAV57808	Human papillomavir
43	320	37.6	1587	18	AAV57808	Human papillomavir
44	310	36.4	1150	22	AAV57808	Human papillomavir
45	197	23.1	119	22	AAV57808	Polyepitope polype

ALIGNMENTS

RESULT 1  
AAV57808  
ID AAV57808 standard; peptide: 151 AA.  
XX AC AAV57808;  
DT 20-MAR-2000 (first entry).  
XX DE HPV-16 E6 protein amino acid sequence.  
XX KW Transcriptional adaptor motif; TRAM, TRAM interaction motif; TRIM.  
KW creb binding protein; transcriptional regulation; cytosolic; antiviral;  
KW cell cycle inhibitor; viral transcription inhibitor; cancer; tumour;  
KW viral disease; viral infection; cell cycle; apoptosis; growth arrest.  
XX OS Human papillomavirus.  
XX PN WO961608-A2.  
XX PD 02-DEC-1999.  
XX PE 26-MAY-1999; 99MO-GH01668.  
XX PR 26-MAY-1998; 98GB-0011303.  
XX PR 05-JAN-1999; 99GB-0000157.  
XX PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.  
XX PI O'Connor MJ, Zimmermann H;  
XX DR WPI; 2000-072620/06.  
XX PT Novel polypeptides cells useful for treating viral disease and cancer

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:45 ; Search time 24.0859 Seconds  
(without alignments)  
420.734 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFQDPERPRKLPOLCTELQ.....WTGRMCCRRSRRTRETQL 151

Scoring table: BLOSUM62

Gap 10.0 , Gapext 0.5

Searched: 239201 seqs, 67110966 residues

Total number of hits satisfying chosen parameters: 239201

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending\_Patents\_AA\_New.\*

1: /cgn2\_6/ptodata/1/paa/PCF\_NEW\_COMB.pep.\*  
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7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	851	100.0	151	5	US-09-701-080C-18
2	843	99.1	273	5	US-09-581-976B-4
3	843	99.1	292	5	US-09-581-976B-10
4	843	99.1	371	5	US-09-581-976B-6
5	843	99.1	390	5	US-09-581-976B-14
6	833	97.9	151	6	US-10-177-390-6
7	469.5	55.2	278	5	US-09-581-976B-21
8	469.5	55.2	383	5	US-09-581-976B-23
9	90.5	10.6	572	6	US-10-240-851-107
10	85	10.0	479	5	US-09-724-676-54539
11	85	10.0	479	5	US-09-724-676-54540
12	85	10.0	479	5	US-09-724-676-54541
13	85	10.0	479	5	US-09-724-676-54542
14	85	10.0	479	5	US-09-724-676-54543
15	85	10.0	479	5	US-09-724-676-54544
16	85	10.0	479	5	US-09-724-676-54545
17	85	10.0	479	5	US-09-724-676-54546
18	85	10.0	479	5	US-09-724-676-54547
19	85	10.0	479	5	US-09-724-676-54548
20	85	10.0	479	5	US-09-724-676-54549
21	85	10.0	479	5	US-09-724-676-54550
22	85	10.0	479	5	US-09-724-676-54551
23	85	10.0	479	5	US-09-724-676-54552
24	85	10.0	479	5	US-09-724-676-54553
25	85	10.0	479	5	US-09-724-676-54554
26	85	10.0	479	5	US-09-724-676-54555

27	85	10.0	479	5	US-09-724-676A-54547	Sequence 54547, A
28	85	10.0	513	5	US-09-724-676-54554	Sequence 54554, A
29	85	10.0	513	5	US-09-724-676-54555	Sequence 54555, A
30	85	10.0	513	5	US-09-724-676-54556	Sequence 54556, A
31	85	10.0	513	5	US-09-724-676-54557	Sequence 54557, A
32	85	10.0	513	5	US-09-724-676-54558	Sequence 54558, A
33	85	10.0	513	5	US-09-724-676-54559	Sequence 54559, A
34	85	10.0	513	5	US-09-724-676-54560	Sequence 54560, A
35	85	10.0	513	5	US-09-724-676-54561	Sequence 54561, A
36	85	10.0	513	5	US-09-724-676-54562	Sequence 54562, A
37	85	10.0	513	5	US-09-724-676A-54554	Sequence 54554, A
38	85	10.0	513	5	US-09-724-676A-54555	Sequence 54555, A
39	85	10.0	513	5	US-09-724-676A-54556	Sequence 54556, A
40	85	10.0	513	5	US-09-724-676A-54557	Sequence 54557, A
41	85	10.0	513	5	US-09-724-676A-54558	Sequence 54558, A
42	85	10.0	513	5	US-09-724-676A-54559	Sequence 54559, A
43	85	10.0	513	5	US-09-724-676A-54560	Sequence 54560, A
44	85	10.0	513	5	US-09-724-676A-54561	Sequence 54561, A
45	85	10.0	513	5	US-09-724-676A-54562	Sequence 54562, A

## ALIGNMENTS

```

RESULT 1
US-09-701-080C-18
; Sequence 18, Application US/09701080C
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF MOLECULAR AND CELL BIOLOGY
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P30
; FILE REFERENCE: N73477C GCM
; CURRENT APPLICATION NUMBER: US/09/701,080C
; PRIOR FILING DATE: 2001-02-27
; PRIOR APPLICATION NUMBER: GB 9811303.8
; PRIOR FILING DATE: 1998-05-26
; PRIOR APPLICATION NUMBER: GB 9900157.0
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 18
; LENGTH: 151
; TYPE: PRT
; ORGANISM: Human papillomavirus
US-09-701-080C-18

Query Match      100.0%; Score 851; DB 5; Length 151;
Best Local Similarity 100.0%; Pred. No. 2.6e-84;
Matches 151; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MFQDPERPRKLPOLCTELQTTIHDIILRCVYCKQOLLREYVDFAFRDICTIYRDGNY 60
        |||||||
DB      61 AVDCDKLTKYSKSEYRHCYSLYGFTLGGYAKPKPLCDLIRINCOKPLCEPKORHD 120
        |||||||
QY      61 AVDCDKLTKYSKSEYRHCYSLYGFTLGGYAKPKPLCDLIRINCOKPLCEPKORHD 120
        |||||||
DB      61 AVDCDKLTKYSKSEYRHCYSLYGFTLGGYAKPKPLCDLIRINCOKPLCEPKORHD 120
        |||||||
QY      121 KQRFNINRGWTRGMSCCRRSRRTRETQL 151
        |||||||
DB      121 KQRFNINRGWTRGMSCCRRSRRTRETQL 151
        |||||||

RESULT 2
US-09-581-976B-4
; Sequence 4, Application US/09581976B
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976B
; CURRENT FILING DATE: 2000-06-20

```

```

? PRIOR APPLICATION NUMBER: PCT/EP98/08563
? PRIOR FILING DATE: 1998-12-18
? PRIOR APPLICATION NUMBER: GB 9727262.9
? PRIOR FILING DATE: 1997-12-24
? NUMBER OF SEQ ID NOS: 28
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4
? LENGTH: 273
? TYPE: PRT
? ORGANISM: Artificial Sequence
? FEATURE:
? OTHER INFORMATION: Chimaeeric protein (protein D from Haemophilus
? OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type
? OTHER INFORMATION: 16)
? OS-09-581-976b-4

```

Query Match	99.1%	Score 843;	DB 5;	Length 273;
Best Local Similarity	99.3%	Pred. No. 3.4e-83;		
Matches 150;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0

QY	1	MEODPEERPRLLPOLCJELQJTTIDHILLECVCCKOQLLRREVDYFAFRDLCIYVROSNPY	60
Db	114	MEODPEERPRLLPOLCJELQJTTIDHILLECVCCKOQLLRREVDYFAFRDLCIYVROSNPY	173
QY	61	AVCCKCLKEFYSKYESEYHRYCYSLGTGLLEDOYKNPCLDILIRCIINCKRPLCPREKORHLD	120
Db	174	AVCCKCLKEFYSKYESEYHRYCYSLGTGLLEDOYKNPCLDILIRCIINCKRPLCPREKORHLD	233
QY	121	KKORPHNIRGWTGRCMSCCSSRTRRETOJL	151
Db	234	KKORPHNIRGWTGRCMSCCSSRTRRETOJL	264

RESULT 3  
HS-09-581-976B-10

```

Sequence 10, Application US/09581976B
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J
APPLICANT: Gerard, Catherine Marie Ghislaine
TITLE OR INVENTION: Vaccine
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976B
CURRENT FILING DATE: 2000-06-20
PRIOR APPLICATION NUMBER: PCT/EP98/08563
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: GB 97/27262.9
PRIOR FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 10
LENGTH: 292
TYPE: PR1
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chlamaic protein (Clyta from Streptococcus
OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus
OTHER INFORMATION: 16)
OS-09-581-976B-10

```

Query Match	99.18;	Score 843;	DB 5;	length 292;
Best Local Similarity	99.38;	Pred. No. 3.6e-83;		
Matches 150;	Conservative	0;	Mismatches 1;	Indels 0
				Gaps 0

QY	1	MFQOPQRPRLPOLCJELQTTIDIIILECYACQOQLIREVYDFARDCIAYRQGNPY	60
Db	133	MFQOPQRPRLPOLCJELQTTIDIIILECYACQOQLIREVYDFARDCIAYRQGNPY	1922
QY	61	AVCDCKLFYSKYSEYRHYCYSLYGTITLLEOYNKPLCDLIRICINCKPLCPBEKQNHLD	120
Db	193	AVCDCKLFYSKYSEYRHYCYSLYGTITLLEOYNKPLCDLIRICINCKPLCPBEKQNHLD	2522
QY	121	KQGFHNIRGHWIGRMSCCRSSYTRRETOU	151

Db 253 KQRFHNRGRWTGRCMSCCRSSRTRETQ 283

RESULT 4  
HS-09-581-976B-6

```

Sequence 6, Application US/095811976B
GENERAL INFORMATION:
APPLICANT: Dalemans, Wilfried L.J.
APPLICANT: Gerard, Catherine Marie Chislaïne
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45124
CURRENT APPLICATION NUMBER: US/09/581,976B
CURRENT FILING DATE: 2000-06-20
PRIORITY APPLICATION NUMBER: PCT/JP98/08563
PRIORITY FILING DATE: 1998-12-18
PRIORITY APPLICATION NUMBER: GB 9727262.9
PRIORITY FILING DATE: 1997-12-24
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 6
LENGTH: 371
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: ChimERIC protein (protein D from Haemophilus
OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma
OTHER INFORMATION: virus type 16)
IS-09-581-976B-

```

Query Match	99.1%	Score 843;	DB 5;	Length 371;
Best Local Similarity	99.3%	Pred. NO. 4.5e-83;		
Matches 150; Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;

	QY	Db	QY	Db	QY	Db	QY	Db
1	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	60	1	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	60	1	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	60
114	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	173	114	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	173	114	MFODRBRPRKLPOLCSTELQTTTHDILLECVCYCKQQLBREYVDFARDCIYRGSPNY	173
61	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	120	61	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	120	61	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	120
174	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	233	174	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	233	174	AVCDCKLKFYSKYSEYHNYCYSLVGTTLLEOYNKPLCDDLRCINCKPLCPREKORHLD	233
121	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	151	121	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	151	121	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	151
234	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	264	234	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	264	234	KKQRFHNIIRGHWTCRMCSSCRSSRTRETOJ	264

RESULT 5  
US-09-581-976B-14

APPLICANT: Daelemans, Wilfried L.J.  
 APPLICANT: Gerard, Catherine Marie Ghislaine  
 TITLE OF INVENTION: Vaccine  
 FILE REFERENCE: B45124  
 CURRENT APPLICATION NUMBER: US/09/581.9768  
 CURRENT FILING DATE: 2000-06-20  
 PRIOR APPLICATION NUMBER: PCT/EP98/08563  
 PRIOR FILING DATE: 1998-12-18  
 PRIOR APPLICATION NUMBER: GB 9727262.9  
 PRIOR FILING DATE: 1997-12-24  
 NUMBER OF SEQ ID NOS: 28  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO 14  
 LENGTH: 390  
 TYPE: PRT  
 ORGANISM: Artificial Sequence  
 FEATURE:  
 OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus  
 OTHER INFORMATION: pneumoniae and E6E7 fusion from human papilloma  
 OTHER INFORMATION: virus type 16)  
 OS-09-581-976B-14

Query Match 99.18; Score 843; DB 5; Length 390;

Best Local Similarity 99.3%; Pred. No. 4.7e-83;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOODPERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 60  
 DB 133 MFOODPERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 192  
 QY 61 AVCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 120  
 DB 193 AVCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 252  
 QY 121 KQRFHNINGRMTGRCMSCCRSSRTRETOL 151  
 DB 253 KQRFHNINGRMTGRCMSCCRSSRTRETOL 283

RESULT 6  
 US-10-177-390-6  
 ; Sequence 6, Application US/10177390  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Schuler, Gerold  
 ; APPLICANT: N.V. Antwerp's Innovatiecentrum  
 ; TITLE OF INVENTION: Improved transfection of Eucaryotic Cells with linear  
 ; FILE REFERENCE: 021505wo/3H/ml  
 ; CURRENT APPLICATION NUMBER: US/10/177,390  
 ; CURRENT FILING DATE: 2002-06-20  
 ; NUMBER OF SEQ ID NOS: 34  
 ; SOFTWARE: PatentIn Ver. 2.1  
 ; SEQ ID NO 6  
 ; LENGTH: 151  
 ; TYPE: PRP  
 ; ORGANISM: Human papillomavirus type 16  
 US-10-177-390-6

Query Match 97.9%; Score 833; DB 6; Length 151;  
 Best Local Similarity 98.0%; Pred. No. 2.3e-82;  
 Matches 148; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFOODPERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 60  
 DB 1 MFOODPERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 60  
 QY 61 AVCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 120  
 DB 61 AVCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 120  
 QY 121 KQRFHNINGRMTGRCMSCCRSSRTRETOL 151  
 DB 121 KQRFHNINGRMTGRCMSCCRSSRTRETOL 151

RESULT 7  
 US-09-581-976B-21  
 ; Sequence 21, Application US/09581976B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dalemans, Wilfried L.J.  
 ; APPLICANT: Gerard, Catherine Marie Ghislaine  
 ; TITLE OF INVENTION: Vaccine  
 ; FILE REFERENCE: B45124  
 ; CURRENT APPLICATION NUMBER: US/09/581,976B  
 ; CURRENT FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
 ; PRIOR FILING DATE: 1998-12-18  
 ; PRIOR APPLICATION NUMBER: GB 9727262.9  
 ; PRIOR FILING DATE: 1997-12-24  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 21  
 ; LENGTH: 278  
 ; TYPE: PRP  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:

; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus  
 ; OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type  
 ; OTHER INFORMATION: 18)  
 US-09-581-976B-21

Query Match 55.2%; Score 469.5; DB 5; Length 278;  
 Best Local Similarity 56.1%; Pred. No. 5.2e-43;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FODPOERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 61  
 DB 115 FODPOERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 174  
 QY 62 VCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 121  
 DB 175 ACHKCIDFYSKIRLEIRHNSDSYGTLEKLTITGYNLLIRCLROCKPLNPAEKLRHLINE 234  
 QY 122 KQRFHNINGRMTGRCMSCCRSSR-----TRETOL 151  
 DB 235 KQRFHNINGRMTGRCMSCCRSSR-----TRETOL 269

RESULT 8  
 US-09-581-976B-23  
 ; Sequence 23, Application US/09581976B  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Dalemans, Wilfried L.J.  
 ; APPLICANT: Gerard, Catherine Marie Ghislaine  
 ; TITLE OF INVENTION: Vaccine  
 ; FILE REFERENCE: B45124  
 ; CURRENT APPLICATION NUMBER: US/09/581,976B  
 ; CURRENT FILING DATE: 2000-06-20  
 ; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
 ; PRIOR FILING DATE: 1998-12-18  
 ; PRIOR APPLICATION NUMBER: GB 9727262.9  
 ; PRIOR FILING DATE: 1997-12-24  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 23  
 ; LENGTH: 383  
 ; TYPE: PRP  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Chimaeic protein (protein D from Haemophilus  
 ; OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma  
 ; OTHER INFORMATION: virus type 18)  
 US-09-581-976B-23

Query Match 55.2%; Score 469.5; DB 5; Length 383;  
 Best Local Similarity 56.1%; Pred. No. 7.1e-43;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FODPOERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 61  
 DB 115 FODPOERPRKLPOLCTELQTTIHDIILECYCKOOLLREYDFAFRDLCTIYRDGNPY 174  
 QY 62 VCDKCLFKYSKYSEYRHYCSLYGTTLEQOYNKPLCDLLIRINCINQKPLCEPEKORHLD 121  
 DB 175 ACHKCIDFYSKIRLEIRHNSDSYGTLEKLTITGYNLLIRCLROCKPLNPAEKLRHLINE 234  
 QY 122 KQRFHNINGRMTGRCMSCCRSSR-----TRETOL 151  
 DB 235 KQRFHNINGRMTGRCMSCCRSSR-----TRETOL 269

RESULT 9  
 US-10-240-851-107  
 ; Sequence 107, Application US/10240851  
 ; GENERAL INFORMATION:  
 ; APPLICANT: John P. Carulli et al.  
 ; TITLE OF INVENTION: THE HIGH BONE MASS GENE OF 11q13.3  
 ; FILE REFERENCE: 032796-021  
 ; CURRENT APPLICATION NUMBER: US/10/240,851

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; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: US 09/544,398
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/543,771
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 09/229,319
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/071,449
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: US 60/105,511
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 109
; SEQ ID NO 107
; LENGTH: 572
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-240-851-107
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Query Match 10.6%; Score 90.5; DB 6; Length 572;
Best Local Similarity 23.5%; Pred. No. 0.062;
Matches 43; Conservative 20; Mismatches 65; Indels 55; Gaps 11;
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OY 1 MFQD---PQRPRKLPDLC-----TELOTTHDIIIECVYCKQOLLREYV 43
DB 366 LMDMEHPQONAVANELGCRHQPLARAQPAVARALGOLFHIACFTCHOCAGQOQFY 425
OY 44 DFAFRDLCI-VYRD-----GNPYAVCDKLFYKSEYRHYCS-----LYGTT 87
DB 426 SLEGAPRCCEGYDTLEKTCGEP---ITRMLRATCK--AYPHCTCYVVCARPLEGTS 481
OY 88 -LEQYKPKLC-----DLLIRICINCKPLCPE---EKORHLDKKORFHNIRGRTGRC 136
DB 482 FIYDQANRPKCPVDYHKKQYAPRCSCSEPIPERGDETVRVVALDKNFHM-----KC 534
OY 137 MSC 139
DB 535 YKC 537
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```
RESULT 10
US-09-724-676-54539
; Sequence 54539, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54539
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54539
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
```

```
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCTELQTTIHDIILIECVYCKQOLLREYVDFAFRDLCIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVYTAGKWTWHPHFVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREKORHLDK 121
DB 380 SPRCYVC-----NGPILDKVVTALDRTWHPHFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 11
US-09-724-676-54540
; Sequence 54540, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54540
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54540
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCTELQTTIHDIILIECVYCKQOLLREYVDFAFRDLCIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVYTAGKWTWHPHFVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREKORHLDK 121
DB 380 SPRCYVC-----NGPILDKVVTALDRTWHPHFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 12
US-09-724-676-54541
; Sequence 54541, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 54541
; LENGTH: 479
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-54541
```

```
Query Match 10.0%; Score 85; DB 5; Length 479;
```

```
Best Local Similarity 19.9%; Pred. No. 0.2;
Matches 30; Conservative 22; Mismatches 41; Indels 58; Gaps 7;
```

```
OY 14 QLCTELQTTIHDIILIECVYCKQOLLREYVDFAFRDLCIYRDGNPYAVCDKLFYKSKY 73
DB 334 QVYTAGKWTWHPHFVCTHGOEIGSRNFE-----RDGQPY--CEK--DYHNLF 379
OY 74 SEYRHYCYSLYGTTLLEQYKPKPLCDLLIR-----CINCKPLCPREKORHLDK 121
DB 380 SPRCYVC-----NGPILDKVVTALDRTWHPHFCAQCGAFGPE----- 419
OY 122 KORFHNIRGR-----WTGRMSSCCRS 142
DB 420 --GFHEKDGKAYCRKDYFDMFAPKCGGCARA 448
```

```
RESULT 13
US-09-724-676-54542
; Sequence 54542, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
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GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: December 13, 2002, 08:37:10 : Search time 252.902 Seconds  
(without alignments)  
384.951 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFQDPERRKLPQLCTELQ.....WTGRCSGCCRSRRRTRETQL 151

## Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

## Database :

Pending\_Patents\_AA\_Main:\*

1: /cgn2\_6/ptodata/1/paa/PCRTUS.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/paa/US06.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/paa/US07.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/paa/US08.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/paa/US081.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/paa/US082.COMB.pep:\*  
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11: /cgn2\_6/ptodata/1/paa/US087.COMB.pep:\*  
12: /cgn2\_6/ptodata/1/paa/US088.COMB.pep:\*  
13: /cgn2\_6/ptodata/1/paa/US089.COMB.pep:\*  
14: /cgn2\_6/ptodata/1/paa/US090.COMB.pep:\*  
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16: /cgn2\_6/ptodata/1/paa/US092.COMB.pep:\*  
17: /cgn2\_6/ptodata/1/paa/US093.COMB.pep:\*  
18: /cgn2\_6/ptodata/1/paa/US094.COMB.pep:\*  
19: /cgn2\_6/ptodata/1/paa/US095.COMB.pep:\*  
20: /cgn2\_6/ptodata/1/paa/US096.COMB.pep:\*  
21: /cgn2\_6/ptodata/1/paa/US097.COMB.pep:\*  
22: /cgn2\_6/ptodata/1/paa/US098.COMB.pep:\*  
23: /cgn2\_6/ptodata/1/paa/US099.COMB.pep:\*  
24: /cgn2\_6/ptodata/1/paa/US100.COMB.pep:\*  
25: /cgn2\_6/ptodata/1/paa/US101.COMB.pep:\*  
26: /cgn2\_6/ptodata/1/paa/US102.COMB.pep:\*  
27: /cgn2\_6/ptodata/1/paa/US60.COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	851	100.0	151	21	US-09-701-080A-18
2	843	99.1	158	1	PCT-US00-33549-31
3	843	99.1	158	23	US-09-980-523A-2
4	843	99.1	273	19	US-09-581-976-4
5	843	99.1	273	24	US-10-000-903-4
6	843	99.1	292	19	US-09-581-976-10

	7	8	843	99.1	292	24	US-10-000-903-10	Sequence 10, Appl
	8	843	99.1	371	19	US-09-581-976-6	Sequence 6, Appl	
	9	843	99.1	371	24	US-10-000-903-6	Sequence 6, Appl	
	10	843	99.1	390	19	US-09-581-976-14	Sequence 14, Appl	
	11	843	99.1	390	24	US-10-000-903-14	Sequence 14, Appl	
	12	840	98.7	151	27	US-60-306-809-20	Sequence 20, Appl	
	13	840	98.7	151	27	US-60-415-929-13	Sequence 13, Appl	
	14	840	98.7	248	27	US-60-415-929-13	Sequence 1, Appl	
	15	835	98.1	248	27	US-60-415-929-7	Sequence 7, Appl	
	16	833	97.9	151	15	US-09-177-390-6	Sequence 6, Appl	
	17	816	95.9	248	27	US-60-415-929-3	Sequence 3, Appl	
	18	816	95.9	248	27	US-60-415-929-5	Sequence 5, Appl	
	19	811	95.3	248	27	US-60-415-929-9	Sequence 9, Appl	
	20	811	95.3	248	27	US-60-415-929-11	Sequence 11, Appl	
	21	799.5	93.9	243	18	US-09-462-993-1	Sequence 1, Appl	
	22	538	63.2	149	1	PCT-US00-33549-45	Sequence 45, Appl	
	23	534	62.7	149	1	PCT-US00-33549-58	Sequence 58, Appl	
	24	469.5	55.2	158	1	PCT-US00-33549-38	Sequence 38, Appl	
	25	469.5	55.2	158	5	US-08-176-937A-4	Sequence 4, Appl	
	26	469.5	55.2	278	19	US-09-581-976-21	Sequence 21, Appl	
	27	469.5	55.2	278	24	US-10-000-903-21	Sequence 21, Appl	
	28	469.5	55.2	383	19	US-09-581-976-23	Sequence 23, Appl	
	29	469.5	55.2	383	24	US-10-000-903-23	Sequence 23, Appl	
	30	460.5	54.1	158	1	PCT-US00-33549-51	Sequence 51, Appl	
	31	441.5	51.9	155	1	PCT-US00-33549-63	Sequence 63, Appl	
	32	332	39.0	236	1	PCT-US00-25559-157	Sequence 157, App	
	33	332	39.0	236	20	US-09-664-225-157	Sequence 157, App	
	34	332	39.0	237	1	PCT-US00-25559-158	Sequence 158, App	
	35	332	39.0	237	20	US-09-664-225-158	Sequence 158, App	
	36	332	39.0	261	1	PCT-US00-25559-160	Sequence 160, App	
	37	332	39.0	161	20	US-09-664-225-160	Sequence 160, App	
	38	331	38.9	117	31	PCT-US00-25559-126	Sequence 126, App	
	39	331	38.9	117	20	US-09-664-225-126	Sequence 126, App	
	40	321	37.7	150	1	PCT-US00-33549-6	Sequence 6, Appl	
	41	320	37.6	150	1	PCT-US00-33549-15	Sequence 15, Appl	
	42	320	37.6	368	14	US-09-000-004-20	Sequence 20, Appl	
	43	320	37.6	375	14	US-09-000-004-22	Sequence 22, Appl	
	44	320	37.6	465	14	US-09-000-004-24	Sequence 24, Appl	
	45	320	37.6	1587	14	US-09-000-004-46	Sequence 46, Appl	

## ALIGNMENTS

RESULT 1  
US-09-701-080A-18  
; Sequence 18, Application US/09701080A  
; GENERAL INFORMATION:  
; APPLICANT: O'CONNOR, MARK J.  
; APPLICANT: ZIMMERMAN, HOLGER  
; TITLE OF INVENTION: POLYPEPTIDES FROM CREB BINDING PROTEIN AND RELATED PROTEIN P30  
; FILE REFERENCE: 117-328  
; CURRENT APPLICATION NUMBER: US/09/701,080A  
; CURRENT FILING DATE: 2001-02-27  
; PRIOR APPLICATION NUMBER: GB 9811303.8  
; PRIOR FILING DATE: 1998-05-26  
; PRIOR APPLICATION NUMBER: GB 9900157.0  
; PRIOR FILING DATE: 1999-01-05  
; NUMBER OF SEQ ID NOS: 36  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 18  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-09-701-080A-18

Query Match 100.0% Score 851: DB 21: Length 151:  
Best Local Similarity 100.0%: Pred. No. 1e-80:  
Matches 151: Conservative 0: Mismatches 0: Indels 0: Gaps 0:  
1 MFQDPERRKLPQLCTELQTHDIIECVCKQKQLRREYDFAFDLCIVYRDGPNY 60  
|||||

Db 1 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 60  
QY 61 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 120  
Db 61 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 120  
QY 121 KKORFNHNRGRMTGRMCSRSSRTRETOL 151  
Db 121 KKORFNHNRGRMTGRMCSRSSRTRETOL 151

RESULT 2  
PCT-US00-33549-31  
Sequence 31, Application PC/TUS0033549

GENERAL INFORMATION:  
APPLICANT: Sette, Alessandro  
APPLICANT: Sidney, John  
APPLICANT: Southwood, Scott  
APPLICANT: Chesnut, Robert  
APPLICANT: Cells, Esteban  
APPLICANT: Grey, Howard M.  
APPLICANT: Eplimmune Inc.  
TITLE OF INVENTION: Inducing Cellular Immune Responses to Human  
TITLE OF INVENTION: Papillomavirus Using Peptide and Nucleic Acid  
FILE REFERENCE: 018623-016110PC  
CURRENT APPLICATION NUMBER: PCT/US00/33549  
CURRENT FILING DATE: 2000-12-11  
PRIOR APPLICATION NUMBER: US 60/172,705  
PRIOR FILING DATE: 1999-12-10  
PRIOR APPLICATION NUMBER: US 09/641,528  
PRIOR FILING DATE: 2000-08-15  
NUMBER OF SEQ ID NOS: 86  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 31  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Human papillomavirus type 16  
PCT-US00-33549-31

Query Match 99.1%; Score 843; DB 1; Length 158;  
Best Local Similarity 99.3%; Pred. No. 7.3e-80;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 60  
Db 8 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 67  
QY 61 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 120  
Db 68 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 127  
QY 121 KKORFNHNRGRMTGRMCSRSSRTRETOL 151  
Db 128 KKORFNHNRGRMTGRMCSRSSRTRETOL 158

RESULT 3  
US-09-980-523A-2  
Sequence 2, Application US/09980523A  
GENERAL INFORMATION:  
APPLICANT: CHOPIN, JEANNINE  
APPLICANT: BOURGAULT VILLADA, ISABELLE  
APPLICANT: GUILLET, JEAN-GERARD  
APPLICANT: CONNAN, FRANCINE  
APPLICANT: FERRIES, ESTELLE  
TITLE OF INVENTION: POLYPEPTIC PROTEIN FRAGMENTS OF THE E6 AND E7  
TITLE OF INVENTION: PROTEINS OF HPV, THEIR PRODUCTION AND THEIR USE  
FILE REFERENCE: WO/1 AO INS  
CURRENT APPLICATION NUMBER: US/09/980,523A  
CURRENT FILING DATE: 2002-04-29  
PRIOR APPLICATION NUMBER: PCT/FR00/01513

PRIOR FILING DATE: 2000-05-31  
PRIOR APPLICATION NUMBER: FR 99/07012  
PRIOR FILING DATE: 1999-06-03  
NUMBER OF SEQ ID NOS: 24  
SOFTWARE: Patent In Ver. 2.1  
SEQ ID NO 2  
LENGTH: 158  
TYPE: PRT  
ORGANISM: Human Papillomavirus  
US-09-980-523A-2

Query Match 99.1%; Score 843; DB 23; Length 158;  
Best Local Similarity 99.3%; Pred. No. 7.3e-80;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 60  
Db 8 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 67  
QY 61 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 120  
Db 68 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 127  
QY 121 KKORFNHNRGRMTGRMCSRSSRTRETOL 151  
Db 128 KKORFNHNRGRMTGRMCSRSSRTRETOL 158

RESULT 4  
US-09-581-976-4  
Sequence 4, Application US/09581976  
GENERAL INFORMATION:  
APPLICANT: Dalemans, Wilfried L.J.  
APPLICANT: Gerard, Catherine Marie Ghislaine  
TITLE OF INVENTION: Vaccine  
FILE REFERENCE: B45124  
CURRENT APPLICATION NUMBER: US/09/581,976  
CURRENT FILING DATE: 2000-06-20  
PRIOR APPLICATION NUMBER: PCT/EP98/08563  
PRIOR FILING DATE: 1998-12-18  
PRIOR APPLICATION NUMBER: GB 9727262.9  
PRIOR FILING DATE: 1997-12-24  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 4  
LENGTH: 273  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
OTHER INFORMATION: Influenza B and E6 from Human papilloma virus type  
OTHER INFORMATION: 16)  
US-09-581-976-4

Query Match 99.1%; Score 843; DB 19; Length 273;  
Best Local Similarity 99.3%; Pred. No. 1.4e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 60  
Db 114 MFODPOERPKLPOLCTELQTTIHDIILECYCKQOALLREVDYDFARDLCTIYRDGPNY 173  
QY 61 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 120  
Db 174 AVCDKCLFKFSKYSEYRHHYCSLYGTTLEOYNNKPLCDLLIRNCINCKPILCPPEKORHLD 233  
QY 121 KKORFNHNRGRMTGRMCSRSSRTRETOL 151  
Db 234 KKORFNHNRGRMTGRMCSRSSRTRETOL 264

RESULT 5  
US-10-000-903-4

```
; Sequence 4, Application US/10000903
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 273
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-4

Query Match          99.1%; Score 843; DB 24; Length 273;
Best Local Similarity 99.3%; Pred. No. 1.4e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 114 MFDDPQERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIYRDGNPY 173
QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 120
DB 174 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 233
QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151
DB 234 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 264

RESULT 6
US-09-581-976-10
; Sequence 10, Application US/09581976
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Chafficial Sequence
; FEATURE:
; OTHER INFORMATION: Chimaeric proteain (Clyta from Streptococcus
; OTHER INFORMATION: pneumoniae and E6 from Human papilloma virus type
; OTHER INFORMATION: 16)
US-09-581-976-10

Query Match          99.1%; Score 843; DB 19; Length 292;
Best Local Similarity 99.3%; Pred. No. 1.5e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFDDPQERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIYRDGNPY 60
DB 133 MFDDPQERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIYRDGNPY 192
```

```
QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 120
DB 193 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 252
QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151
DB 253 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 283

RESULT 7
US-10-000-903-10
; Sequence 10, Application US/10000903
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Bernande
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10

Query Match          99.1%; Score 843; DB 24; Length 292;
Best Local Similarity 99.3%; Pred. No. 1.5e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFDDPQERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIYRDGNPY 60
DB 133 MFDDPQERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIYRDGNPY 192
QY 61 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 120
DB 193 AVCDKCLFKFSKSEYRHCYSLYGTTLEQYNNKPLCDLLIRINCINOKPLCEPKORHLD 252
QY 121 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 151
DB 253 KKQRFNINRGWTRGCMSCCRSSRTTRRETOL 283

RESULT 8
US-09-581-976-6
; Sequence 6, Application US/09581976
; GENERAL INFORMATION:
; APPLICANT: Dalemans, Wilfried L.J.
; APPLICANT: Gerard, Catherine Marie Ghislaine
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45124
; CURRENT APPLICATION NUMBER: US/09/581,976
; CURRENT FILING DATE: 2000-06-20
; PRIOR APPLICATION NUMBER: PCT/EP98/08563
; PRIOR FILING DATE: 1998-12-18
; PRIOR APPLICATION NUMBER: GB 9727262.9
; PRIOR FILING DATE: 1997-12-24
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

OTHER INFORMATION: Chimeric protein (protein D from Haemophilus  
; OTHER INFORMATION: Influenza B and E6E7 fusion from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-09-581-976-6

Query Match 99.1%; Score 843; DB 19; Length 371;  
Best Local Similarity 99.3%; Pred. No. 2e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 60  
DB 114 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 173  
QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 120  
DB 174 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 233  
QY 121 KQRFNHRGRWGTGRMCCSCSSRTRETOL 151  
DB 234 KQRFNHRGRWGTGRMCCSCSSRTRETOL 264

RESULT 9  
US-10-000-903-6  
; Sequence 6, Application US/10000903

GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000, 903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 6  
; LENGTH: 371  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-6

Query Match 99.1%; Score 843; DB 24; Length 371;  
Best Local Similarity 99.3%; Pred. No. 2e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 60  
DB 114 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 173  
QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 120  
DB 174 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 233  
QY 121 KQRFNHRGRWGTGRMCCSCSSRTRETOL 151  
DB 234 KQRFNHRGRWGTGRMCCSCSSRTRETOL 264

RESULT 10  
US-09-581-976-14  
; Sequence 14, Application US/09581976  
; GENERAL INFORMATION:  
; APPLICANT: Dalemans, Wilfried L.J.  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45124  
; CURRENT APPLICATION NUMBER: US/09/581, 976

CURRENT FILING DATE: 2000-06-20  
; PRIOR APPLICATION NUMBER: PCT/EP98/08563  
; PRIOR FILING DATE: 1998-12-18  
; PRIOR APPLICATION NUMBER: GB 9727262.9  
; PRIOR FILING DATE: 1997-12-24  
; NUMBER OF SEQ ID NOS: 26  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Chimeric protein (Clyta from Streptococcus  
; OTHER INFORMATION: pneumoniae and E6E7 fusion from Human papilloma  
; OTHER INFORMATION: virus type 16)  
US-09-581-976-14

Query Match 99.1%; Score 843; DB 19; Length 390;  
Best Local Similarity 99.3%; Pred. No. 2.1e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 60  
DB 133 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 192  
QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 120  
DB 193 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 252  
QY 121 KQRFNHRGRWGTGRMCCSCSSRTRETOL 151  
DB 253 KQRFNHRGRWGTGRMCCSCSSRTRETOL 283

RESULT 11  
US-10-000-903-14  
; Sequence 14, Application US/10000903

GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Bernande  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000, 903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 14  
; LENGTH: 390  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-14

Query Match 99.1%; Score 843; DB 24; Length 390;  
Best Local Similarity 99.3%; Pred. No. 2.1e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 60  
DB 133 MFODPOERPRKLPOLCTELQTTIHDIIECYCKQOLLRRVYDFAFRDLCIYRDGPNY 192  
QY 61 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 120  
DB 193 AVCDKCLFYSKYSEYRHYCYSLYGTLLLEQOYNKPLCDLLIRNCINOKPLCPPEKORHLD 252  
QY 121 KQRFNHRGRWGTGRMCCSCSSRTRETOL 151

Db 253 KQRFHNRGRWTGRCMSCRSSRTRRETOL 283

## RESULT 12

US-60-306-809-20  
; Sequence 20, Application US/60306809  
; GENERAL INFORMATION:  
; APPLICANT: SASTRY, K. JAGANNADHA  
; APPLICANT: TORTOLERO-LUNA, GUILLEMO  
; APPLICANT: POLLEN, MICHELE AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO HPV-ASSOCIATED  
; FILE REFERENCE: US/60306809  
; CURRENT FILING DATE: 2001-07-20  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 20  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus  
US-60-306-809-20

Query Match 98.7%; Score 840; DB 27; Length 151;  
Best Local Similarity 98.7%; Pred. No. 1.4e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
DB 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151  
DB 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151

## RESULT 13

US-60-415-929-13  
; Sequence 13, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 13  
; LENGTH: 151  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-13

Query Match 98.7%; Score 840; DB 27; Length 151;  
Best Local Similarity 98.7%; Pred. No. 1.4e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
DB 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151  
DB 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151

## RESULT 14

US-60-415-929-1  
; Sequence 1, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 1  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-1

Query Match 98.7%; Score 840; DB 27; Length 248;  
Best Local Similarity 98.7%; Pred. No. 2.6e-79;  
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
DB 1 MFOQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 60  
QY 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120  
DB 61 AVCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 120

QY 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151  
DB 121 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151

## RESULT 15

US-60-415-929-7  
; Sequence 7, Application US/60415929  
; GENERAL INFORMATION:  
; APPLICANT: Cassetti, Maria  
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS POLYPEPTIDES AND IMMUNOGENIC COMPOSITIONS  
; FILE REFERENCE: 0630/OM137-USO  
; CURRENT FILING DATE: 2002-10-03  
; NUMBER OF SEQ ID NOS: 14  
; SOFTWARE: Patent In version 3.1  
; SEQ ID NO 7  
; LENGTH: 248  
; TYPE: PRT  
; ORGANISM: Human papillomavirus type 16  
US-60-415-929-7

Query Match 98.1%; Score 835; DB 27; Length 248;  
Best Local Similarity 98.7%; Pred. No. 8.7e-79;  
Matches 148; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 FODQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 61  
DB 99 FODQDERPRKLPOLCTELQTTIHDIIECYCKQOLLREYDFAFRDLCTIYRDGNPY 158  
QY 62 VCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 121  
DB 159 VCDKCLKFSYSEYRHHYCSLYGTTLEQOYNKPLCDLLIRINCINOKPLCEPEKORHLD 218  
QY 122 KQRFHNRGRWTGRCMSCRSSRTRRETOL 151  
DB 219 KQRFHNRGRWTGRCMSCRSSRTRRETOL 248

Search completed: December 13, 2002, 08:44:50  
Job time : 253.902 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:20 ; Search time 3.82822 Seconds  
(without alignments)  
645.878 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Listing first 45 summaries

Database :

SPTREMBL\_21:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rotent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	255	10 Q9FRJ9	Q9FRJ9 oryza sativ
2	31	79.5	367	1 Q59667	Q59667 pyrococcus
3	31	79.5	367	17 Q9VOC2	Q9VOC2 pyrococcus
4	31	79.5	367	17 Q8U2E5	Q8U2E5 pyrococcus
5	31	79.5	369	1 Q9UMQ9	Q9UMQ9 thermococcus
6	31	79.5	508	5 Q9XTT3	Q9XTT3 caenorhabdi
7	31	79.5	552	16 Q97EE3	Q97EE3 clostridium
8	30	76.9	119	5 Q9XWV9	Q9XWV9 caenorhabdi
9	30	76.9	144	16 Q9KJ2	Q9KJ2 vibrio chol
10	30	76.9	148	17 Q9YFK5	Q9YFK5 aetopyrum p
11	30	76.9	157	5 Q9BIM1	Q9BIM1 giardia lam
12	30	76.9	165	3 Q12157	Q12157 saccharomye
13	30	76.9	198	16 Q9KVL1	Q9KVL1 vibrio chol
14	30	76.9	204	10 Q9JUL6	Q9JUL6 arabidopsis
15	30	76.9	210	10 Q9FHG8	Q9FHG8 arabidopsis
16	30	76.9	214	11 Q9DIY0	Q9DIY0 mus musculi

17	30	76.9	232	11 Q9CYU1	Q9CYU1 mus musculi
18	30	76.9	238	10 Q8S2K2	Q8S2K2 oryza sativ
19	30	76.9	238	12 Q8UZN7	Q8UZN7 tobacco str
20	30	76.9	238	12 Q8UYC4	Q8UYC4 tobacco str
21	30	76.9	247	12 Q91MM4	Q91MM4 lumby skin
22	30	76.9	258	4 Q15262	Q15262 homo sapien
23	30	76.9	258	4 Q9NMW3	Q9NMW3 homo sapien
24	30	76.9	297	12 Q9YH65	Q9YH65 melanoplus
25	30	76.9	300	17 Q97OR9	Q97OR9 sulfobolus
26	30	76.9	300	17 Q97YV0	Q97YV0 sulfobolus
27	30	76.9	306	17 Q9HM25	Q9HM25 thermoplasm
28	30	76.9	306	17 Q97C08	Q97C08 thermoplasm
29	30	76.9	329	3 Q9P7F8	Q9P7F8 schizosach
30	30	76.9	335	17 Q27446	Q27446 methanobact
31	30	76.9	343	10 Q9C9X1	Q9C9X1 arabidopsis
32	30	76.9	343	11 Q9DBH5	Q9DBH5 mus musculi
33	30	76.9	348	17 Q50099	Q50099 pyrococcus
34	30	76.9	349	10 Q9SU66	Q9SU66 arabidopsis
35	30	76.9	352	17 Q27796	Q27796 methanobact
36	30	76.9	356	10 Q9XJ08	Q9XJ08 oryza sativ
37	30	76.9	362	10 Q9M2E6	Q9M2E6 arabidopsis
38	30	76.9	376	10 Q9FL07	Q9FL07 arabidopsis
39	30	76.9	379	10 Q93YQ5	Q93YQ5 arabidopsis
40	30	76.9	381	10 Q9CAM6	Q9CAM6 arabidopsis
41	30	76.9	381	10 Q93Z65	Q93Z65 arabidopsis
42	30	76.9	406	10 Q9LR95	Q9LR95 arabidopsis
43	30	76.9	407	10 Q9C965	Q9C965 arabidopsis
44	30	76.9	408	10 Q9LN71	Q9LN71 arabidopsis
45	30	76.9	452	4 Q9NMA5	Q9NMA5 homo sapien

#### ALIGNMENTS

RESULT 1  
Q9FRJ9 PRELIMINARY: PRT: 255 AA.  
ID Q9FRJ9  
AC Q9FRJ9  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Putative ring finger protein.  
GN OSUNB0064P21.7.  
OS Oryza sativa (Rice).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC Ehrhartoideae; Oryzeae; Oryza.  
OX NCBI\_TaxID=4530;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CV. NIPPONBARE;  
RA Buell C.R., Yuan Q., Moffat K.S., Hill J.N., Burr P.C., Hsiao J.,  
RA Zisman V., Pal G., Bowman C.L., Fujii C.Y., VanAken S.E.,  
RA Bowman C.L., Craven B., Utterback T.R., Khalak H., Feldblum T.V.,  
RA Quackenbush J., White O., Salzberg S.L., Fraser C.M.;  
RT "Oryza sativa chromosome 10 BAC OSUNB0064P21 genomic sequence.";  
RL Submitted (Aug-2001) to the EMBL/GenBank/DBJ databases.  
CC -i- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
DR EMBL: AC073166; AAC46117.1; -  
DR InterPro: IPR001841; Znf.Fing.  
DR Pfam: PF00097; zfc3HC4; 1.  
DR SMART: SM00184; RING; 1.  
KW Zinc-finger.  
SQ SEQUENCE 255 AA: 25099 MW: 66F94C3C7C987412 CRC64;

Query Match 79.5%; Score 31; DB 10; Length 255;  
Best Local Similarity 57.1%; Pred. No. 1.4e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 193 NSSCPSC 199

RESULT 2  
059667  
ID 059667 PRELIMINARY; PRT; 367 AA.  
AC 059667;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Hydrogenase (alpha subunit) (EC 1.12.2.1).  
GN HYD (ALPHA SUBUNIT).  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 3638;  
RX MEDLINE=95219100; PubMed=7704275;  
RA Pedroni P., Della Volpe A., Gaili G., Mura G.M., Pratesi C.,  
RA Grandi G.;  
RT "Characterization of the locus encoding the [Ni-Fe] sulfhydrogenase  
from the archaeon Pyrococcus furiosus: evidence for a relationship to  
bacterial sulfate reductases";  
RL Microbiology 141:449-458(1995).  
DR EMBL; X75255; CA53034.1; -;  
DR InterPro; IPR001450; 4Fe4S\_Ferredoxin.  
DR Pfam; PF00037; fer4; 1.  
DR PROSITE; PS00198; 4Fe4S\_FERREDOXIN; 2.  
KW Oxidoreductase.  
SQ SEQUENCE 367 AA; 43398 MW; 9E1509580310330 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246  
RESULT 3  
09VOC2  
ID 09VOC2 PRELIMINARY; PRT; 367 AA.  
AC 09VOC2;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
DE Hydrogenase (EC 1.12.2.1) (Cytochrome-C3 hydrogenase beta chain).  
GN PAB1784.  
OS Pyrococcus abyssi.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=29292;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-ORSAY;  
RA Heilig R.;  
RT "Pyrococcus abyssi genome sequence: insights into archaeal chromosome  
structure and evolution.";  
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AJ248285; CAB49782.1; -;  
DR InterPro; IPR001450; 4Fe4S\_Ferredoxin.  
DR PROSITE; PS00198; 4Fe4S\_FERREDOXIN; 2.  
KW Complete proteome.  
SQ SEQUENCE 367 AA; 43230 MW; 7D2F51C7F846BC0C CRC64;

Query Match 79.5%; Score 31; DB 17; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246

RESULT 4  
0802E5  
ID 0802E5 PRELIMINARY; PRT; 367 AA.  
AC 0802E5;  
DT 01-JUN-2002 (TREMBLrel. 21, Created)  
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
DE Sulfhydrogenase beta subunit.  
GN PF0891.  
OS Pyrococcus furiosus.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Pyrococcus.  
OX NCBI\_TaxID=2261;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-VCI / DSM 3638 / ATCC 43587 / JCM 8422;  
RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;  
RT "The complete sequence of the Pyrococcus furiosus genome";  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF010204; AAL81015.1; -;  
KW Complete proteome.  
SQ SEQUENCE 367 AA; 43398 MW; 8329F3842CB48D0 CRC64;

Query Match 79.5%; Score 31; DB 17; Length 367;  
Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTTCPTC 246  
RESULT 5  
09UWQ9  
ID 09UWQ9 PRELIMINARY; PRT; 369 AA.  
AC 09UWQ9;  
DT 01-MAY-2000 (TREMBLrel. 13, Created)  
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE Nife hydrogenase beta subunit.  
GN HYD.  
OS Thermococcus litoralis.  
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;  
OC Thermococcus.  
OX NCBI\_TaxID=2265;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-DSM 4573;  
RX MEDLINE=20050631; PubMed=10583413;  
RA Rakhely G., Zhou Z.Z., Adams M.W.W., Kovacs K.L.;  
RT "Biochemical and molecular characterization of the [Nife] hydrogenase  
from the hyperthermophilic archaeon, Thermococcus litoralis";  
RL Eur. J. Biochem. 266:1158-1165(1999).  
DR EMBL; AF039208; AAB94933.1; -;  
DR InterPro; IPR001450; 4Fe4S\_Ferredoxin.  
DR Pfam; PF00037; fer4; 1.  
DR PROSITE; PS00198; 4Fe4S\_FERREDOXIN; 2.  
SQ SEQUENCE 369 AA; 43293 MW; 42332FEB7D749973 CRC64;

Query Match 79.5%; Score 31; DB 1; Length 369;  
Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 242 NTTCPTC 248  
RESULT 6  
09XTT3  
ID 09XTT3 PRELIMINARY; PRT; 508 AA.

AC Q9XWT3;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Y49E10.20 protein.  
 GN Y49E10.20.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Barlow K.;  
 RL Submitted (Aug-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT Investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; 298866; CAB11566.2; -;  
 DR InterPro: IPR002159; CD36.  
 DR Pfam: PF01130; CD36; 1.  
 DR PRINTS: PR01609; CD36FAMILY.  
 SQ SEQUENCE 508 AA; 57287 MW; 5A7078A78F599806 CRC64;

Query Match 79.5%; Score 31; DB 5; Length 508;  
 Best Local Similarity 57.1%; Pred. No. 2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 Db 135 NASCPXC 141

RESULT 7  
 O97EE3 PRELIMINARY; PRT; 552 AA.  
 AC O97EE3;  
 DT 01-OCT-2001 (TREMBLrel. 18, Created)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Dihydroxy-acid dehydratase.  
 GN CAC3170.  
 OS Clostridium acetobutylicum.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;  
 OC Clostridiales; Clostridiaceae; Clostridium.  
 OC NCBI\_TaxID=1488;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;  
 RX MEDLINE=2159325; PubMed=11466286;  
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,  
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hittl J., Wolf Y.I.,  
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,  
 RA Bennett G.N., Koonin E.V., Smith D.R.,  
 "Genome sequence and comparative analysis of the solvent-producing  
 RT bacterium Clostridium acetobutylicum".  
 RL J. Bacteriol. 183:4823-4838(2001).  
 DR EMBL; AE007812; AAK81107.1; -;  
 DR InterPro: IPR004404; ILVD.  
 DR InterPro: IPR000581; ILVD\_EDD\_family.  
 DR Pfam: PF00920; ILVD\_EDD; 1.  
 DR ProDom: PD002691; ILVD\_EDD\_family; 1.  
 DR TIGRFAMS: TIGR00110; ILVD; 1.  
 DR PROSITE: PS00886; ILVD\_EDD\_1; 1.  
 DR PROSITE: PS00887; ILVD\_EDD\_2; 1.  
 KM Complete proteome.  
 SQ SEQUENCE 552 AA; 58366 MW; 9309A73FE7CD81F5 CRC64;

Query Match 79.5%; Score 31; DB 16; Length 552;  
 Best Local Similarity 57.1%; Pred. No. 2e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 4 NXXCPXC 10  
 Db 182 NTACPC 188

RESULT 8  
 O9XW9 PRELIMINARY; PRT; 119 AA.  
 AC O9XW9;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 DE T28C6.8 protein.  
 GN T28C6.8.  
 OS Caenorhabditis elegans.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
 OC Rhabditidae; Peloderinae; Caenorhabditis.  
 OC NCBI\_TaxID=6239;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Lloyd C.R.;  
 RL Submitted (SEP-1995) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=99069613; PubMed=9851916;  
 none;  
 RT "Genome sequence of the nematode C.elegans: A platform for  
 RT Investigating biology."  
 RL Science 282:2012-2018(1998).  
 DR EMBL; 254238; CAA90999.2; -;  
 SQ SEQUENCE 119 AA; 13204 MW; E7127E4547880432 CRC64;

Query Match 76.9%; Score 30; DB 5; Length 119;  
 Best Local Similarity 57.1%; Pred. No. 1.3e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 Db 8 NNSCPAC 14

RESULT 9  
 O9KJ2 PRELIMINARY; PRT; 144 AA.  
 AC O9KJ2;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Thioresdoxin 2.  
 GN VCA0752.  
 OS Vibrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 OC NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=EL TOR N16961 / SEROTYPE O1;  
 RX MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eissen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 RA Ermolaeva M.D., Yamashiro J., Bass S., Qin H., Dragoi I., Sellers P.,  
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 RA Fraser C.M.;  
 "DNA sequence of both chromosomes of the cholera pathogen Vibrio  
 RT cholerae".  
 RL Nature 406:477-483(2000).  
 DR EMBL; AE004403; AAF96650.1; -;  
 DR HSSP: P80579; IQOW.  
 DR TIGR: VCA0752; -;  
 DR InterPro: IPR000063; Thioresdoxin.

DR Pfam; PF00085; thiorid. 1.  
 DR PRINTS; PR00421; THIORIDOXIN.  
 DR TIGRFAMs; TIGR01068; thioridoxin. 1.  
 KM Complete proteome.  
 SQ SEQUENCE 144 AA; 15968 MW; 9997AF6744A84CA5 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 144;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 5 NTRCPC 11

## RESULT 10

O9YFK5 PRELIMINARY; PRT; 148 AA.

AC O9YFK5;  
 DT 01-NOV-1999 (TREMBlrel. 12, Created)  
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein APE0243.  
 GN APE0243.  
 OS Aeropyrum pernix.  
 OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcaceae;  
 OC Desulfurococcaceae; Aeropyrum.  
 OX NCBI\_TaxID=56636;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K1;  
 RX MEDLINE=99310339; PubMed=10382966;  
 RA Kwarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Halkawa Y.,  
 RA Jin-no K., Takahashi M., Sekine M., Baba S.-I., Akai A., Kosugi H.,  
 RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,  
 RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,  
 RA Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Kubota K.,  
 RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.,  
 RT "Complete genome sequence of an aerobic hyper-thermophilic  
 RT crenarchaeon, Aeropyrum pernix K1.",  
 RL DNA Res. 6:83-101(1999)  
 DR EMBL; AP000058; BAK79156.1; -.  
 DR InterPro: IPR000063; Thiorid.  
 KM Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 148 AA; 16500 MW; 263ABD8E89307F CRC64;

Query Match 76.9%; Score 30; DB 17; Length 148;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 50 NALCPAC 56

## RESULT 11

O9BIM1 PRELIMINARY; PRT; 157 AA.

AC O9BIM1;  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Variable surface protein 7b (Fragment).  
 OS Giardia lamblia (Giardia intestinalis).  
 OC Eukaryota; Diplomonadida; Hexamitidae; Giardinae; Giardia.  
 OX NCBI\_TaxID=5741;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21391783; PubMed=11500396;  
 RA Blenz M., Siles-lucas M., Wittner P., Muller N.,  
 RT "vsp Gene Expression by Giardia lamblia Clone GS/M-83-H7 during  
 RL Infect. Immun. 69:5278-5285(2001)."

DR EMBL; AF354520; AAK31225.1; -.  
 DR InterPro: IPR005127; Giardia\_vsp.  
 DR Pfam; PF03302; VSP; 1.  
 FT NON TER 1  
 FT NON TER 157  
 SQ SEQUENCE 157 AA; 15872 MW; 8C370EF98907D76B CRC64;

Query Match 76.9%; Score 30; DB 5; Length 157;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 44 NGSCPAC 50

## RESULT 12

O12157 PRELIMINARY; PRT; 165 AA.

AC O12157;  
 DT 01-NOV-1996 (TREMBlrel. 01, Created)  
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
 DE Chromosome IV reading frame ORF YDL008W.  
 GN APC11 OR D2900 OR YDL008W.  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Urrestarazu L.A., Andre B., Vissers S.,  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MIPS;  
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ALPHA S288C;  
 RA Andre B., Vissers S., Urrestarazu L.,  
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; Z74056; CAA98564.1; -.  
 DR EMBL; Z48432; CAA88351.1; -.  
 DR SGD; S0002166; APC11.  
 DR InterPro: IPR001841; Znf\_ring.  
 DR SMART; SM00184; RING; 1.  
 KM Hypothetical protein.  
 SQ SEQUENCE 165 AA; 18865 MW; 99F8E8C6B841934 CRC64;

Query Match 76.9%; Score 30; DB 3; Length 165;  
 Best Local Similarity 57.1%; Pred. No. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
 | | | |  
 Db 49 NGTCCPC 55

## RESULT 13

O9KVL1 PRELIMINARY; PRT; 198 AA.

AC O9KVL1;  
 DT 01-OCT-2000 (TREMBlrel. 15, Created)  
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)  
 DE Hypothetical protein VC0131.  
 GN VC0131.  
 OS Vibrrio cholerae.  
 OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrrio.  
 OX NCBI\_TaxID=666;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-EL TOR N16961 / SEROTYPE O1;  
 RA MEDLINE=20406833; PubMed=10952301;  
 RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,  
 Dodson R.J., Hart D.H., Hickey E.K., Peterson J.D., Umayam L.A.,  
 Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,  
 Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragol I., Sellers P.,  
 McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,  
 Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,  
 Fraser C.M.,  
 RT "DNA sequence of both chromosomes of the cholera pathogen vibrio  
 cholerae";  
 RL Nature 406:477-483(2000).  
 DR EMBL: AE004103; AAF93308.1;  
 DR TIGR: VC0131;  
 DR InterPro: IPR000152; ASX\_Hydroxyl;  
 DR PROSITE: PS00010; ASX\_HYDROXYL; UNKNOWN\_1.  
 KW Hypothetical protein; Complete proteome.  
 SQ SEQUENCE 198 AA; 22841 MW; C139FCAAE26F3A7 CRC64;

Query Match 76.9%; Score 30; DB 16; Length 198;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 1 1 1 1  
 DB 2 NACCPDC 8

## RESULT 14

Q9JUL6 PRELIMINARY; PRT; 204 AA.

AC Q9JUL6;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Similarity to RING-H2 zinc finger protein ATL3.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.;  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.  
 RM [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE=20277480; PubMed=10819329;  
 RA Nakamura Y.;  
 RT "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence  
 RT features of the regions of 4,504,864 bp covered by sixty p1 and TAC  
 RT clones.";  
 RL DNA Res. 7:131-135(2000).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AB022220; BAB01038.1; -;  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW zinc-finger.  
 SQ SEQUENCE 204 AA; 22859 MW; 90FC33157DA90D25 CRC64;

Query Match 76.9%; Score 30; DB 10; Length 204;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 1 1 1 1  
 DB 123 NSTCPIC 129

## RESULT 15

Q9FHG8 PRELIMINARY; PRT; 210 AA.

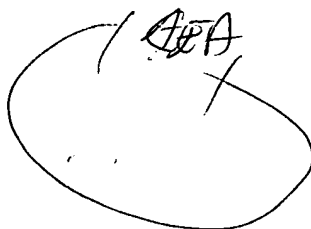
AC Q9FHG8;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE Similarity to C3HC4-type RING zinc finger protein.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-COLUMBIA;  
 RX MEDLINE=99397451; PubMed=10470850;  
 RA Kaneko T., Katoh T., Sato S., Nakamura Y., Asamizu E., Kotani H.,  
 Miyajima N., Tabata S.;  
 RL "Structural analysis of Arabidopsis thaliana chromosome 5. IX.  
 RL Sequence features of the regions of 1,011,550 bp covered by seventeen  
 RL p1 and TAC clones.";  
 RL DNA Res. 6:183-195(1999).  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 DR EMBL: AB018118; BAB09593.1; -;  
 DR InterPro: IPR001841; Znf\_ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 KW zinc-finger.  
 SQ SEQUENCE 210 AA; 23523 MW; E27A1C1A75CC77A6 CRC64;

Query Match 76.9%; Score 30; DB 10; Length 210;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 1 1 1 1  
 DB 157 NSTCPIC 163

Search completed: December 13, 2002, 08:39:37  
 Job time : 6.82822 secs

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102(a)

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:40 ; Search time 1.25153 Seconds

(without alignments)  
397.685 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 45 summaries

Database : SWISSPROT\_40:\*

Result No. Score Query Match Length DB ID

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# SUMMARIES

Description

1 31 79.5 286 1 ILVD\_CLOPA

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22 31 79.5 286 1 ILVD\_CLOPA

23 31 79.5 286 1 ILVD\_CLOPA

24 31 79.5 286 1 ILVD\_CLOPA

25 31 79.5 286 1 ILVD\_CLOPA

26 31 79.5 286 1 ILVD\_CLOPA

27 31 79.5 286 1 ILVD\_CLOPA

28 31 79.5 286 1 ILVD\_CLOPA

29 31 79.5 286 1 ILVD\_CLOPA

30 31 79.5 286 1 ILVD\_CLOPA

31 31 79.5 286 1 ILVD\_CLOPA

32 31 79.5 286 1 ILVD\_CLOPA

33 31 79.5 286 1 ILVD\_CLOPA

## ALIGNMENTS

34 29 74.4 233 1 HOXU\_ALCEU P22318 alca1genes  
35 29 74.4 281 1 VNS1\_INBAC P13883 influenza b  
36 29 74.4 281 1 VNS1\_INBAC P12592 influenza b  
37 29 74.4 281 1 VNS1\_INBAC P12594 influenza b  
38 29 74.4 281 1 VNS1\_INBID P12596 influenza b  
39 29 74.4 281 1 VNS1\_INB5J P12601 influenza b  
40 29 74.4 281 1 VNS1\_INB5J P12602 influenza b  
41 29 74.4 281 1 VNS1\_INB5J P12603 influenza b  
42 29 74.4 333 1 Y808\_METTA Q58218 methanococc  
43 29 74.4 377 1 R8G1\_HUMAN Q06587 homo sapien  
44 29 74.4 421 1 R8G1\_METTA Q58239 methanococc  
45 29 74.4 459 1 ZPR1\_MOUSE Q62384 mus musculu

## RESULT 1

ILVD\_CLOPA STANDARD: PRT: 286 AA.

AC P31959: 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)

DE 15-JUN-2002 (Rel. 41, Last annotation update)

NE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD) (Fragment).

ILVD.

CC Clostridium pasteurianum.

CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;

CC Clostridium.

CC NCBI\_TaxID=1501;

CC SEQUENCE FROM N.A.

CC MEDLINE=94227243; PubMed=8173074;

CC Oultram J.D., Loughlin M., Wainman S.M., Minton N.P.;

CC "The nucleotide sequence of genes involved in the leucine

CC biosynthetic pathway of Clostridium pasteurianum."

CC DNA Seq. 4:105-111(1993).

CC -1- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate -> 3-methyl-2-

CC oxobutanoate + H2O.

CC -1- CORFACTOR: BINDS 1 4FE-4S CLUSTER (POTENTIAL).

CC -1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.

CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.

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CC EMBL: L06666; AAC4195.1;

CC InterPro: IPR000581; ILVD\_EDD\_family.

CC Pfam: PF00920; ILVD\_EDD\_1.

CC ProDom: PD002691; ILVD\_EDD\_family; 1.

CC PROSITE: PS00886; ILVD\_EDD\_2; PARTIAL.

CC Branch-chain amino acid biosynthesis; Lyase; Iron-sulfur; 4Fe-4S.

CC METAL 119 119 IRON-SULFUR (4FE-4S) (POTENTIAL).

CC FT METAL 191 191 IRON-SULFUR (4FE-4S) (POTENTIAL).

CC FT NON\_TER 286 286 IRON-SULFUR (4FE-4S) (POTENTIAL).

CC SQ SEQUENCE 286 AA; 29925 MW; 7CF6655CCE927 CRC64;

Query Match Score 31; DB 1; Length 286;

Best Local Similarity 57.1%; Pred. No. 60;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10

DB 182 NXXCPXC 188

RESULT 2

```

ILVD_CLOAB
ID ILVD_CLOAB STANDARD; PRT; 552 AA.
AC 097EE3;
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Dihydroxy-acid dehydratase (EC 4.2.1.9) (DAD).
GN ILVD OR CAC3170.
OS Clostridium acetobutylicum.
OC Bacteria: Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=11359325; Pubmed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Qiu D., Hiltl J., Wolf Y.I.,
RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum."
RT J. Bacteriol. 183:4823-4838(2001).
CC -1- CATALYTIC ACTIVITY: 2,3-dihydroxy-3-methylbutanoate = 3-methyl-2-
CC Oxobutanate + H(2)O.
CC -1- COFACTOR: Binds 1 4Fe-4S cluster (Potential).
CC -1- PATHWAY: Valine and isoleucine biosynthesis; fourth step.
CC -1- SIMILARITY: BELONGS TO THE ILVD / EDD FAMILY.
CC -----
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CC -----
CC EMBL; AE007812; AAK8107.1; -.
CC DR InterPro: IPR004404; ILVD.
CC DR InterPro: IPR000581; ILVD_EDD_family.
CC DR Pfam: PF00920; ILVD_EDD_1.
CC DR ProDom: PD002691; ILVD_EDD_family; 1.
CC DR TIGRfam: TIGR00110; ILVD_1.
CC DR PROSITE: PS00886; ILVD_EDD_1; 1.
CC DR PROSITE: PS00887; ILVD_EDD_2; 1.
CC KM Branched-chain amino acid biosynthesis; Lyase; Iron-sulfur; 4Fe-4S;
CC Complete proteome.
CC FT METAL 119 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC FT METAL 191 IRON-SULFUR (4FE-4S) (POTENTIAL).
CC SQ SEQUENCE 552 AA; 58366 MW; 9309A73FE7CD81F5 CRC64;
Query Match 79.5%; Score 31; DB 1; Length 552;
Best Local Similarity 57.1%; Pred. No. 93;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 NXXCPXC 10
Db 182 NTACPTC 188

```

```

RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88004470; Pubmed=3308458;
RA Cole S.T.;
RT "Nucleotide sequence and comparative analysis of the ftd operon
RT encoding the fumarate reductase of Proteus vulgaris. Extensive
RT sequence divergence of the membrane anchors and absence of an
RT ftd-linked ampc cephalosporinase gene."
RL Eur. J. Biochem. 167:481-488(1987).
CC -1- FUNCTION: PROBABLY PLAYS A ROLE IN AN HYDROGENASE NICKEL COFACTOR
CC INSERTION STEP.
CC -1- SIMILARITY: BELONGS TO THE HYPA/HYBF FAMILY.
CC -----
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CC -----
CC EMBL; X06151; CAA29510.1; -.
CC DR PIR; S00118; S00118.
CC DR InterPro: IPR000688; HyPA.
CC DR Pfam; PF01155; HyPA; 1.
CC DR ProDom; PD003620; HyPA; 1.
CC DR TIGRfam; TIGR00100; hyPA; 1.
CC DR PROSITE: PS01249; HyPA; 1.
CC KM Metal-binding; Nickel.
CC FT METAL 2 NICKEL (POTENTIAL).
CC FT METAL 73 NICKEL (POTENTIAL).
CC FT METAL 76 NICKEL (POTENTIAL).
CC FT METAL 89 NICKEL (POTENTIAL).
CC FT METAL 92 NICKEL (POTENTIAL).
CC SQ SEQUENCE 113 AA; 12619 MW; 17C4D73C6A1B2DD CRC64;
Query Match 76.9%; Score 30; DB 1; Length 113;
Best Local Similarity 57.1%; Pred. No. 46;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 NXXCPXC 10
Db 86 MAGCPAC 92

```

```

RESULT 4
COAT_TOBSV
ID COAT_TOBSV STANDARD; PRT; 237 AA.
AC P03598;
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE Coat protein (p4 protein).
OS Tobacco streak virus (strain WC) (TSV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Bromoviridae;
OC Ilarivirus.
OX NCBI_TaxID=12318;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84169544; Pubmed=6546793;
RA cornelissen B.J.C., Janssen H., Zuidema D., Bol J.F.;
RT "Complete nucleotide sequence of tobacco streak virus RNA 3."
RT Nucleic Acids Res. 12:2427-2437(1984).
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CC -----
CC EMBL; X00435; CAA25133.1; -.

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DR PIR: A04206; VCBWVC.  
 DR InterPro: IPR002681; I1ar-coat.  
 DR Pfam: PF01787; I1ar-coat.1.  
 SO SEQUENCE 237 AA; 26237 MW; E1FF87AE7102523 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 76;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
 DB 25 NSRCPTC 31

RESULT 5  
 LEPA\_PSEAE STANDARD; PRT; 290 AA.  
 AC P22610;  
 DT 01-NOV-1991 (Rel. 19, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Type 4, prepilin-like proteins leader peptide processing enzyme  
 DE (protein secretion protein XCPA) (PILD protein). [Includes: Leader  
 DE peptidase (EC 3.4.99.-) (Prepilin peptidase); N-methyltransferase  
 DE (EC 2.1.1.-)].  
 GN PILD OR XCPA OR PA4528.  
 OS Pseudomonas aeruginosa.  
 OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
 OC Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-PAK:  
 RX MEDLINE=90264276; PubMed=1971619;  
 RA Nunn D., Bergman S., Lory S.;  
 RT "Products of three accessory genes, pilB, pilC, and pILD, are  
 RT required for biogenesis of Pseudomonas aeruginosa pili.";  
 RL J. Bacteriol. 172:2911-2919(1990).  
 RN (2)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PAO1.  
 RX MEDLINE=91100333; PubMed=1898929;  
 RA Bally M., Ball G., Badere A., Lazdunski A.;  
 RT "Protein secretion in Pseudomonas aeruginosa: the xcpA gene encodes  
 RT an integral inner membrane protein homologous to Klebsiella  
 RT pneumoniae secretion function protein PUO.";  
 RL J. Bacteriol. 173:479-486(1991).  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ATCC 15692 / PAO1.  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrenner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Goltzy L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
 RT "Complete genome sequence of Pseudomonas aeruginosa PAO1, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 RN (4)  
 RP REVIEW.  
 RX MEDLINE=97368114; PubMed=9224881;  
 RA Lory S., Strom M.S.;  
 RT "Structure-function relationship of type-IV prepilin peptidase of  
 RT Pseudomonas aeruginosa -- a review.";  
 RL Gene 192:117-121(1997).  
 RN (5)  
 RP REVIEW.  
 RX MEDLINE=94335721; PubMed=8057924;  
 RA Strom M.S., Nunn D.N., Lory S.;  
 RT "Posttranslational processing of type IV prepilin and homologs by PILD  
 RT of Pseudomonas aeruginosa.";

RL Meth. Enzymol. 235:527-540(1994).  
 RN (6)  
 RP MUTAGENESIS OF CYSTEINE RESIDUES.  
 RX MEDLINE=93340186; PubMed=8340405;  
 RA Strom M.S., Bergman P., Lory S.;  
 RT "Identification of active-site cysteines in the conserved domain of  
 RT PILD, the bifunctional type IV pilin leader  
 RT peptidase/N-methyltransferase of Pseudomonas aeruginosa.";  
 RL J. Biol. Chem. 268:15788-15794(1993).  
 RN (7)  
 RP MUTAGENESIS OF GLY-95 AND LYS-96.  
 RX MEDLINE=98334648; PubMed=9668097;  
 RA Pepe J.C., Lory S.;  
 RT "Amino acid substitutions in pILD, a bifunctional enzyme of  
 RT Pseudomonas aeruginosa. Effect on leader peptidase and  
 RT N-methyltransferase activities in vitro and in vivo.";  
 RL J. Biol. Chem. 273:19120-19129(1998).  
 CC -I- FUNCTION: CLEAVES TYPE-4 FIMBRIAL LEADER SEQUENCE AND METHYLATES  
 CC THE N-TERMINAL (GENERALLY PHE) RESIDUE. PROCESSES THE PILIN  
 CC PRECURSOR DURING MEMBRANE TRANSLOCATION. REQUIRED FOR THE ASSEMBLY  
 CC OF TYPE IV PILI AND FOR SECRETION OF MOST PROTEINS.  
 CC -I- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.  
 CC -I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24.  
 CC -----  
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 CC -----  
 DR EMBL: M32066; AAA25734.1; -  
 DR EMBL: M61096; AAA26023.1; -  
 DR EMBL: AE004867; AAG07916.1; -  
 DR PIR: C35384; C35384.  
 DR PIR: A39131; A39131.  
 DR MEROPS: A24.001; -  
 DR InterPro: IPR000045; Peptidase\_C20.  
 DR Pfam: PF01478; Peptidase\_C20; I.  
 DR PRINTS: PR00864; PREPILNPASE.  
 KW Multifunctional enzyme; Hydrolase; Protease; Transferase;  
 KW Methyltransferase; Transmembrane; Inner membrane; Complete proteome.  
 FT TRANSMEM 13  
 FT DOMAIN 34 127  
 FT TRANSMEM 128 148  
 FT TRANSMEM 158 178  
 FT TRANSMEM 183 203  
 FT TRANSMEM 228 248  
 FT TRANSMEM 261 276  
 FT ACT\_SITE 72 72  
 FT ACT\_SITE 75 75  
 FT ACT\_SITE 97 97  
 FT ACT\_SITE 100 100  
 FT VARIANT 18 18  
 SO SEQUENCE 290 AA; 31870 MW; 57A8526EB18F752 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 290;  
 Best Local Similarity 57.1%; Pred. No. 87;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10  
 DB 69 NSACPCX 75

RESULT 6  
 YDRD\_SCHPO STANDARD; PRT; 547 AA.  
 ID YDRD\_SCHPO  
 AC O13747;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Hypothetical RING finger protein C16B8.13 in chromosome I.  
GN SPAC16B8.13.  
OS Schizosaccharomyces pombe (Fission yeast).  
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;  
OC Schizosaccharomycetales; Schizosaccharomycetaceae;  
OC Schizosaccharomyces.  
OX NCBI\_TaxID=4896;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=972;  
RX MEDLINE=21848401, PubMed=11859360;  
RA Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A.,  
RA Spours J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,  
RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,  
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,  
RA Gaitley S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G.,  
RA Holtroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,  
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,  
RA Mooney P., Moule S., Mungall K., Murphy L., Niblett D., Odell C.,  
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabinovitch E.,  
RA Rutherford K., Rutter S., Saunders R., Seeger K., Sharp S.,  
RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,  
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,  
RA Woodward J., Volckaert G., Aert R., Robben J., Glynnopres B.,  
RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,  
RA Gabel C., Fuchs M., Filtz C., Holzer E., Moestl D., Hilbert H.,  
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,  
RA Egger P., Zimmermann W., Medler H., Wambutt R., Purnelle B.,  
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Leleure V., Motier S.,  
RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,  
RA Lucas M., Roche M., Galliard C., Tallada V.A., Garzon A., Thode G.,  
RA Dada R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,  
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,  
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,  
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;  
RL "The genome sequence of Schizosaccharomyces pombe.";  
RL Nature 415:871-880(2002).  
CC -1- SIMILARITY: TO YEAST YH010C AND C.ELEGANS EEBD8.9.  
CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
CC -----  
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CC -----  
DR EMBL, Z98529, CAB1041.1, -,  
DR InterPro, IPR001607, Znf\_UBP,  
DR InterPro, IPR001841, Znf\_Ring,  
DR Pfam, PF000097, zf-C3HC4, 1,  
DR Pfam, PF02148, zf-UBP, 1,  
DR SMART, SM00184, RING, 1,  
DR SMART, SM00290, Znf\_UBP, 1,  
DR PROSITE, PS00518, ZF\_RING\_1, FALSE\_NEG,  
DR PROSITE, PS50089, ZF\_RING\_2, 1,  
KW Hypothetical protein: Zinc-finger.  
FT ZN\_FING 208 248 RING-TYPE.  
FT DOMAIN 526 534 POLY-UB.  
FT SEQUENCE 547 AA: 61825 MW: 263FBD4ED7CE70E1 CRC64;

```

Query Match          76.9%;  Score 30;  DB 1;  Length 547;
Best Local Similarity 57.1%;  Pred. No. 1.3e+02;
Matches      4;  Conservative      0;  Mismatches      3;  Indels      0;  Gaps      0;

Oy      4  NXXCPCXC  10
        |||||
Db      241  NSSCPVC 247

RESULT 7
RN12_MOUSE

```

ID	RNA2.MCISE	STANDARD:	PRF:	600 AA.
AC	OSM7V7:			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	RING finger protein 12 (LIM domain interacting RING finger protein)			
DE	(RING finger LIM domain-binding protein) (R-LIM).			
CN	RNL2 OR RLIM.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCHI_Taxid=10090;			
RA	[1]			
RP	SEQUENCE FROM N.A.			
RA	Bach I.;			
RT	"Opposing developmental functions of positive and negative			
RT	coregulators of LIM homeodomain factors.";			
RL	Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE=99364422; PubMed=10431247;			
RA	Bach I., Rodriguez-Esteban C., Carriere C., Bhushan A., Krones A.,			
RA	Rose D.W., Glass C.K., Andersen B., Izpisua Belmonte J.C.,			
RA	Rosenfeld M.G.;			
RT	"Rim inhibits functional activity of LIM homeodomain transcription			
RT	factors via recruitment of the histone deacetylase complex.";			
RL	Nat. Genet. 22:394-399(1999).			
CC	-1- FUNCTION: ACQS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN			
CC	TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE			
CC	DEACETYLASE COREPRESSOR COMPLEX.			
CC	-1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.			
CC	-1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.			
CC	-----			
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CC	-----			
DR	EMBL; AF065992; AAC34209.1; -			
DR	MCD; MGI:1342291; Rnfl2.			
DR	InterPro; IPR001841; Znf_ring.			
DR	Pfam; PF00097; zf-C3HC4; 1.			
DR	SMART; SM00184; RING_1.			
DR	PROSITE; PS00518; zf_RING_1; FALSE_NEG.			
DR	PROSITE; PS50089; zf_RING_2; 1.			
KW	Transcription regulation; Zinc-finger.			
FT	DOMAIN 415 .. 484			
FT	FT ZN_FING 546 .. 587			
FT	DOMAIN 447 .. 461			
FT	POLY-SER.			
SEQ	SEQUENCE 600 AA; 66470 MW; E68299530126E41D CRC64;			
Query Match	76.9%;	Score 30;	DB 1;	Length 600;
Similarity	57.1%;	Pred. NO. 1.4e+02;		
Matches	4; Conservative	0; Mismatches	3; Indels	0; Gaps

```

Query Match          76.9%; Score 30; DB 1; Length 600;
Best Local Similarity 57.1%; Pred. No. 1.4e+02;
Matches      4; Conservative      0; Mismatches      3; Indels      0; Gaps      0;

OY      4 NXXCPXC 10
        | | | |
Db      580 NSTCPC 586

RESULT 8
EX02_BP75
ID_EX02_BP75      STANDARD;      PRT;      612 AA.
AC      P11109;
DT      01-JUL-1989 (Rel. 11, Created)
DT      01-JUL-1989 (Rel. 11, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Probable exonuclease subunit 2 (EC 3.1.11.-) (D13).
GN      D13.
OS      Bacteriophage T5.

```

OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae;  
 OC T5-like viruses.  
 OC NCBI\_TaxID=10726;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89057468; PubMed=3057441;  
 RA Kallman A.V., Kryukov V.M., Bayer A.A.;  
 RT "The nucleotide sequence of the region of bacteriophage T5 early  
 RT genes D10-D15.";  
 RL Nucleic Acids Res. 16:10353-10354(1988).  
 RN [2]  
 RP POSSIBLE FUNCTION.  
 RX MEDLINE=89338712; PubMed=2547651;  
 RA Blinov V.M., Koonin E.V., Gorbaleva A.E., Kallman A.V., Kryukov V.M.;  
 RT "Two early genes of bacteriophage T5 encode proteins containing an  
 RT NTP-binding sequence motif and probably involved in DNA replication,  
 RT recombination and repair.";  
 RL FEBS Lett. 252:47-52(1989).  
 CC -1- FUNCTION: POSSIBLE EXONUCLEASE INVOLVED IN PHAGE DNA  
 CC RECOMBINATION, REPLICATION, AND REPAIR.  
 CC -1- SUBUNIT: COULD CONSISTS OF TWO SUBUNITS: D13 AND D12.  
 CC -1- SIMILARITY: STRONG TO T4 PROTEIN GP46.  
 CC -----  
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 CC -----  
 DR EMBL: X12930; CAA31400.1; -;  
 DR EMBL: X12930; CAA31401.1; ALT\_INIT.  
 DR EMBL: AJ001191; CAA04586.1; -;  
 DR FIR: S01933; M0BPT3.  
 DR InterPro: IPR003439; ABC\_transprot.  
 DR Hydrolyase; Nuclease; Exonuclease; ATP-binding; DNA repair;  
 KW Early protein.  
 FT NP\_BIND 35 42 ATP (POTENTIAL).  
 SO SEQUENCE 612 AA; 68673 MW; 92E7B652D1DE141 CRC64;  
 OY 4 NXXCPXC 10  
 DB 306 NTECPXC 312  
 RESULT 9  
 RN12\_HUMAN STANDARD: PRT; 624 AA.  
 ID RN12\_HUMAN  
 AC Q9NW22; Q9Y598;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE RING finger protein 12 (LIM domain interacting RING finger protein)  
 DE (RING finger LIM domain-binding protein) (R-LIM) (NY-RFN-43 antigen).  
 GN RNF12 OR RLIM.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=20469411; PubMed=11013082;  
 OS Ostendorf H.P., Bossenz M., Mincheva A., Copeland N.G., Gilbert D.J.,  
 RA Jenkins N.A., Lichter P., Bach I.;  
 RT "Functional characterization of the gene encoding RLIM, the  
 RT corepressor of LIM homeodomain transcription factors.";  
 RL Genomics 69:120-130(2000).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RC TISSUE=renal cell carcinoma;  
 RX MEDLINE=99438124; PubMed=10508479;  
 RA Scanlan M.J., Jordan J.D., Williamson B., Stockert E., Bander N.H.,  
 RA Jongseneel V., Gure A.O., Jager D., Jager E., Knuth A., Chen Y.-T.,  
 RA Old L.J.;  
 RT "Antigens recognized by autologous antibody in patients with renal-  
 RT cell carcinoma.";  
 RL Int. J. Cancer 83:456-464(1999).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,  
 RA Nishikawa T., Nagai K., Sugano S., Shiratori A., Sudo H.,  
 RA Magatsuma M., Hosoi T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,  
 RA Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,  
 RA Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,  
 RA Yamamoto J., Wakamatsu A., Nakamura Y., Nagahara K., Masuho Y.,  
 RA Nimomiya K., Iwayanagi T.;  
 RT "NED0 human cDNA sequencing project.";  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: ACTS AS A NEGATIVE CO-REGULATOR FOR LIM HOMEODOMAIN  
 CC TRANSCRIPTION FACTORS. VIA THE RECRUITMENT OF THE SIN3A/HISTONE  
 CC DEACETYLASE COREPRESSOR COMPLEX.  
 CC -1- SUBUNIT: ASSOCIATES WITH LIM/HOMEOBOX FACTORS.  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES.  
 CC -1- SIMILARITY: CONTAINS 1 RING-TYPE ZINC FINGER.  
 CC -1- CAUTION: Ref.2 sequence differs from that shown due to frameshifts  
 CC in position 134 and 142.  
 CC -----  
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 CC -----  
 DR EMBL: AJ271670; CAC14228.1; -;  
 DR EMBL: AF155109; AAD42875.1; ALT\_FRAME.  
 DR EMBL: AK001334; BAA91632.1; -;  
 DR Genew; HGNC:13429; RNF12.  
 DR MIM: 300379; -;  
 DR InterPro: IPR001841; Znf\_Ring.  
 DR Pfam: PF00097; zf-C3HC4; 1.  
 DR SMART: SM00184; RING; 1.  
 DR PROSITE: PS00518; ZF\_RING\_1; FALSE\_NEG.  
 DR PROSITE: PS50089; ZF\_RING\_2; 1.  
 KW Transcription regulation; Zinc-finger.  
 FT DOMAIN 422 506  
 FT ZN\_FING 570 611  
 FT DOMAIN 453 481  
 FT DOMAIN 500 506  
 FT CONFLICT 126 126  
 FT CONFLICT 134 134  
 FT CONFLICT 144 145  
 FT CONFLICT 418 418  
 SO SEQUENCE 624 AA; 68527 MW; DE3ADE09ACACCF8 CRC64;  
 OY 4 NXXCPXC 10  
 DB 604 NSTCPXC 610  
 RESULT 10  
 ID ASM\_MOUSE STANDARD: PRT; 627 AA.  
 AC ASM\_MOUSE  
 DT 01-OCT-1993 (Rel. 27, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE sphingomyelin phosphodiesterase precursor (EC 3.1.4.12) (acid  
 sphingomyelinase) (asmase).  
 GN SMPD1 OR ASM.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SRRAIN-BALB/C; TISSUE=Liver;  
 RX MEDLINE=93183402; PubMed=1292508;  
 RA Newzeila D., Stoffel W.;  
 RT "Molecular cloning of the acid sphingomyelinase of the mouse and the  
 RT organization and complete nucleotide sequence of the gene.";  
 RL Biol. Chem. Hoppe-Seyler 373:1233-1238(1992).  
 RN [2]  
 RP REVISIONS TO 224-225 AND 384.  
 RA Hofmann K.;  
 RL Submitted (APR-1994) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Strausberg R.;  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: CONVERTS SPHINGOMYELIN TO CERAMIDE. ASM ALSO HAS  
 CC PHOSPHOLIPASE C ACTIVITIES TOWARD 1,2-DIACYLGLYCEROLPHOSPHOCHOLINE  
 CC AND 1,2-DIACYLGLYCEROLPHOSPHOGLYCEROL.  
 CC -1- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acetylphingosine +  
 CC choline phosphate.  
 CC -1- SUBUNIT: MONOMER.  
 CC -1- SUBCELLULAR LOCATION: Lysosomal.  
 CC -1- MISCELLANEOUS: THERE ARE TWO TYPES OF SPHINGOMYELINASES: ASM  
 CC (ACID), AND NSM (NEUTRAL).  
 CC -1- SIMILARITY: BELONGS TO THE ACID SPHINGOMYELINASE FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 SAPOSIN B-TYPE DOMAIN.  
 CC -----  
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 CC -----  
 DR EMBL; Z14252; CAAT78619.1; -;  
 DR EMBL; Z14132; CAAT78506.1; -;  
 DR EMBL; BC011304; AAH11304.1; -;  
 DR PIR; S27392; S27392.  
 DR PIR; S27393; S27393.  
 DR MGD; MGI:98325; Smpd1.  
 DR InterPro: IPR004843; M-peptidase.  
 DR InterPro: IPR004844; S/T-phosphatase.  
 DR InterPro: IPR000004; Saph.  
 DR Pfam: PF00149; Metallophos; 1.  
 DR SMART; SM00118; SAPB; 1.  
 KW Hydrolase; Glycosidase; Lysosome; Glycoprotein; Signal.  
 FT SIGNAL 1 44  
 FT CHAIN 45 627  
 FT DOMAIN 83 167  
 FT CARBOHYD 84 84  
 FT CARBOHYD 173 173  
 FT CARBOHYD 333 333  
 FT CARBOHYD 393 393  
 FT CARBOHYD 518 518  
 FT CARBOHYD 611 611  
 FT CONFLICT 48 48  
 FT CONFLICT 450 450  
 FT SEQUENCE 627 AA; 65927 MW; 0PFC7EA74EB71B91 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 627;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
 Db 84 NLTCPAC 90  
 RESULT 11  
 ID SYLA\_AQUAE STANDARD; PRT; 634 AA.  
 AC 066680;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE leucyl-tRNA synthetase alpha subunit (EC 6.1.1.4) (leucine--tRNA  
 DE ligase alpha subunit) (leuRS).  
 GN LEUS OR AQ\_351.  
 OS Aquifex aeolicus.  
 OC Bacteria; Aquificae; Aquificae (class); Aquificales; Aquificaceae;  
 OC Aquifex.  
 OC NCBI\_TaxID=63363;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SRRAIN-VF5;  
 RX MEDLINE=98196666; PubMed=9537320;  
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,  
 RA Graham D.E., Overbeek R., Shead M.A., Keller M., Aujay M., Huber R.,  
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;  
 RT "The complete genome of the hyperthermophilic bacterium Aquifex  
 RT aeolicus.";  
 RL Nature 392:353-358(1998).  
 CC -1- CATALYTIC ACTIVITY: ATP + L-leucine + tRNA(leu) = AMP +  
 CC diphosphate + L-leucyl-tRNA(leu).  
 CC -1- SUBUNIT: SEEMS TO CONSIST OF AN ALPHA CHAIN AND A BETA CHAIN.  
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.  
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.  
 CC -----  
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 CC -----  
 DR EMBL; AE000685; AAC06643.1; -;  
 DR HSSP; P96142; IGAX.  
 DR InterPro: IPR002302; Leu-tRNAsynth.  
 DR InterPro: IPR002300; tRNA-synt\_1a.  
 DR InterPro: IPR001412; tRNA-synt\_1.  
 DR Pfam; PF00133; tRNA-synt\_1; 1.  
 DR PRINTS; PR00985; tRNA-synthLEU.  
 DR TIGRFAMS; TIGR00396; leuS\_bact; 1.  
 DR PROSITE; PS00178; AA\_tRNA\_LIGASE\_1; 1.  
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;  
 KW Complete proteome.  
 FT SITE 43 51  
 FT SITE 43 51  
 FT SEQUENCE 634 AA; 73989 MW; 0119CA3F7AD18766 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 634;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 501 NLTCPAC 507  
 RESULT 12  
 ID HGL2\_ARATH STANDARD; PRT; 745 AA.  
 AC P46607; O39018;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Homeobox protein GLABRA2 (Homeobox-leucine zipper protein ATHB-10)  
 DE (HD-ZIP protein ATHB-10).  
 GN GL2 OR AT1G79840 OR F19K16.20.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 NC NCBITaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Wassilewskija; TISSUE=Seedling;  
 RX MEDLINE=95011550; PubMed=7926739;  
 RA Rerie W.G., Feldmann K.A., Marks M.D.;  
 RT "The GLABRA2 gene encodes a homeo domain protein required for normal  
 RL trichome development in Arabidopsis.";  
 RN Genes Dev. 8:1388-1399(1994).  
 RP REVISIONS.  
 RA Marks M.D.;  
 RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=96407838; PubMed=8811855;  
 RA di Cristina M., Sessa G., Dolan L., Instrand P., Balma S., Ruberti I.,  
 RA Morelli G.;  
 RT "The Arabidopsis Athb-10 (GLABRA2) is an HD-zip protein required for  
 RL regulation of root hair development.";  
 RL Plant J. 10:393-402(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv. Columbia;  
 RX MEDLINE=21016719; PubMed=11130712;  
 RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,  
 RA White O., Alonso J., Altati H., Araujo R., Bowman C.L., Brooks S.Y.,  
 RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,  
 RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,  
 RA Dunn P., Elgu P., Feldhym T.V., Feng J.-D., Fong B., Fujii C.Y.,  
 RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Huizar L.,  
 RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,  
 RA Kim C.-J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,  
 RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,  
 RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Mafti R., Marzilli A.,  
 RA Miltischer J., Miranda M., Nguyen M., Niemman W.C., Osborne B.I.,  
 RA Pai G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,  
 RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,  
 RA Sun H., Tallon L.J., Tambunga G., Tortum M.J., Town C.D.,  
 RA Usterback T., Van Aken S., Vayenberg M., Vysotskaia V.S., Walker M.,  
 RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;  
 RT "Sequence and analysis of chromosome 1 of the plant Arabidopsis  
 RL thaliana".  
 RL Nature 408:816-820(2000).  
 CC -1- FUNCTION: REQUIRED FOR CORRECT MORPHOLOGICAL DEVELOPMENT AND  
 CC MATURATION OF TRICHOES AS WELL AS FOR NORMAL DEVELOPMENT OF SEED  
 CC COAT MUCIAGE.  
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).  
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING TRICHOES.  
 CC -1- SIMILARITY: BELONGS TO THE HD-ZIP HOMEBOX FAMILY.  
 CC -1- SIMILARITY: CONTAINS 1 HOMEBOX DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 1 START DOMAIN.  
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 CC -----  
 CC EMBL: L32873; AAC0260.1; -  
 CC EMBL: Z54356; CAA9183.1; ALT\_INIT.  
 CC EMBL: AC011717; AAG52245.1; -  
 CC HSP: P01367; IAPL.

DR TRANSFAC; T02961; -  
 DR InterPro: IPR001356; Homeobox.  
 DR InterPro: IPR002913; START.  
 DR Pfam: PF00046; homeobox; 1.  
 DR Pfam: PF01852; START; 1.  
 DR ProDom: PD000010; Homeobox; 1.  
 DR SMART: SM00389; HOX; 1.  
 DR SMART: SM00234; START; 1.  
 DR PROSITE: PS00027; HOMEBOX\_1; 1.  
 DR PROSITE: PS50071; HOMEBOX\_2; 1.  
 DR PROSITE: PS50848; START; 1.  
 KW Homeobox; DNA-binding; Nuclear protein.  
 FT DOMAIN 248 487 START.  
 FT DOMAIN 39 60 ASP/GLU-RICH (ACIDIC).  
 FT DOMAIN 70 87 ASP/GLU-RICH (ACIDIC).  
 FT DNA\_BIND 99 158 HOMEBOX.  
 SQ SEQUENCE 745 AA; 82988 MW; E4AD2DAAC15D5F3 CRC64;  
 Query Match 76.9%; Score 30; DB 1; Length 745;  
 Best Local Similarity 57.1%; Pred. NO. 1.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXKCPXC 10  
 Db 188 NSSCPNC 194  
 RESULT 13  
 ID NEIL\_HUMAN  
 AC 092832; 09Y472;  
 DT 01-NOV-1997 (Rel. 35. Created)  
 DT 16-OCT-2001 (Rel. 40; Last sequence update)  
 DT 15-JUN-2002 (Rel. 41; Last annotation update)  
 DE Protein kinase C-binding protein NEIL1 precursor (NEIL-like protein 1)  
 DE (Nei-related protein 1).  
 GN NEIL1 OR NRPL.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=97131504; PubMed=8975702;  
 RA Watanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,  
 RA Kanemoto N., Nakamura Y., Hirai Y., Maekawa H., Takahashi E.;  
 RT "Cloning and characterization of two novel human cDNAs (NEIL1 and  
 RL NEIL2) encoding proteins with six EGF-like repeats.";  
 RL Genomics 38:273-276(1996).  
 RN [2]  
 RP SEQUENCE OF 383-810 FROM N.A.  
 RA Ting K., Vastardis H., Mulliken J.B., Bertolami C., Wen Z.,  
 RA Young M., Tieu A., Kwong E.;  
 RT "Nei homolog gene expression in craniofacial anomalies.";  
 RL Submitted (Sep-1996) to the EMBL/Genbank/DBJ databases.  
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Secreted (by similarity).  
 CC -1- DISEASE: EXPRESSED IN CRANIOFACIAL ANOMALIES.  
 CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 WFC DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
 CC -1- CAUTION: REF.2 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO FRAMESHIFTS  
 CC IN POSITIONS 427 AND 771.  
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 CC -----

DR EMBL; D83017; BA11680.1; -.  
 DR EMBL; U57523; AAB06946.1; ALT\_FRAME.  
 DR HSSP; P07204; IADX.  
 DR Genew; HGNC:7750; NELL1.  
 DR MIM; 602319; -.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00001; EGF\_like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 3.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWF; 2.  
 DR GlycoProtein; EGF-like domain; Repeat; Signal.  
 KW SIGNAL. 1 16  
 FT CHAIN 17 810 POTENTIAL.  
 FT DOMAIN 81 230 PROTEIN KINASE C-BINDING PROTEIN NELL1.  
 FT DOMAIN 273 331 TSP N-TERMINAL.  
 FT DOMAIN 335 390 VWF 1.  
 FT DOMAIN 391 433 EGF-LIKE 1.  
 FT DOMAIN 434 475 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 476 516 EGF-LIKE 3.  
 FT DOMAIN 515 547 EGF-LIKE 4.  
 FT DOMAIN 549 595 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 596 631 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).  
 FT DOMAIN 632 687 VWF 3.  
 FT DOMAIN 692 750 VWF 4.  
 FT DOMAIN 752 807 VWF 5.  
 FT DISULFID 395 407 BY SIMILARITY.  
 FT DISULFID 401 416 BY SIMILARITY.  
 FT DISULFID 418 432 BY SIMILARITY.  
 FT DISULFID 438 451 BY SIMILARITY.  
 FT DISULFID 445 460 BY SIMILARITY.  
 FT DISULFID 462 474 BY SIMILARITY.  
 FT DISULFID 480 493 BY SIMILARITY.  
 FT DISULFID 487 502 BY SIMILARITY.  
 FT DISULFID 504 515 BY SIMILARITY.  
 FT DISULFID 519 529 BY SIMILARITY.  
 FT DISULFID 523 535 BY SIMILARITY.  
 FT DISULFID 537 546 BY SIMILARITY.  
 FT DISULFID 553 565 BY SIMILARITY.  
 FT DISULFID 560 575 BY SIMILARITY.  
 FT DISULFID 577 594 BY SIMILARITY.  
 FT DISULFID 600 613 BY SIMILARITY.  
 FT DISULFID 607 622 BY SIMILARITY.  
 FT DISULFID 624 630 BY SIMILARITY.  
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 224 224 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 294 294 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 511 511 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 562 562 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 609 609 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 708 708 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 732 732 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 758 758 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CARBOHYD 383 383 N-LINKED (GLCNAC. .) (POTENTIAL).  
 FT CONFLICT 573 573 Y -> D (IN REF. 2).  
 FT CONFLICT 573 573 Y -> H (IN REF. 2).  
 FT CONFLICT 626 626 S -> C (IN REF. 2).  
 SQ SEQUENCE 810 AA; 89606 MW; 549465EA3FAEBD0 CRC64;

Query Match 76.9%; Score 30; DB 1; Length 810;  
 Best Local Similarity 57.1%; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4 NXXPCX 10  
 Db 224 NHTCPTC 230  
 RESULT 14  
 ID NELL1\_RAT STANDARD; PRT; 810 AA.  
 AC 062919;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE Protein kinase C-binding protein NELL1 precursor (NEL-like protein 1).  
 GN NELL1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_Taxid=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Sprague-Dawley; TISSUE-Brain;  
 RX MEDLINE=20017976; PubMed=10548494;  
 RA Kuroda S., Oyasu M., Kawakami M., Kanayama N., Tanizawa K., Saito N.,  
 RA Abe T., Matsushashi S., Ting K.;  
 RT "Biochemical characterization and expression analysis of neural  
 RT thrombospondin-1-like proteins NELL1 and NELL2";  
 RL Biochem. Biophys. Res. Commun. 265:79-86(1999).  
 CC -1- SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: CONTAINS 1 TSP N-TERMINAL DOMAIN.  
 CC -1- SIMILARITY: CONTAINS 5 VWF DOMAINS.  
 CC -1- SIMILARITY: CONTAINS 6 EGF-LIKE DOMAINS.  
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 DR EMBL; U48246; AAC72252.1; -.  
 DR HSSP; P35355; IEMN.  
 DR InterPro; IPR000152; Asx\_hydroxyl.  
 DR InterPro; IPR000561; EGF-like.  
 DR InterPro; IPR001881; EGF\_Ca.  
 DR InterPro; IPR001791; Laminin\_G.  
 DR InterPro; IPR003129; TSPN.  
 DR InterPro; IPR001007; VWF\_C.  
 DR Pfam; PF00008; EGF; 4.  
 DR Pfam; PF00093; VWC; 3.  
 DR Pfam; PF02210; TSPN; 1.  
 DR SMART; SM00179; EGF\_CA; 2.  
 DR SMART; SM00001; EGF\_like; 4.  
 DR SMART; SM00282; LamG; 1.  
 DR SMART; SM00210; TSPN; 1.  
 DR SMART; SM00214; VWC; 4.  
 DR PROSITE; PS00010; ASX\_HYDROXYL; 3.  
 DR PROSITE; PS00022; EGF\_1; 1.  
 DR PROSITE; PS01186; EGF\_2; 3.  
 DR PROSITE; PS01187; EGF\_CA; 3.  
 DR PROSITE; PS01208; VWF; 2.  
 KW Glycoprotein; EGF-like domain; Repeat; Signal.  
 FT SIGNAL 1 16 POTENTIAL.  
 FT CHAIN 17 810 PROTEIN KINASE C-BINDING PROTEIN NELL1.  
 FT DOMAIN 81 230 TSP N-TERMINAL.  
 FT DOMAIN 273 331 VWF 1.  
 FT DOMAIN 335 390 VWF 2.

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FT DOMAIN 391 433 EGF-LIKE 1.
FT DOMAIN 475 475 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 476 516 EGF-LIKE 3.
FT DOMAIN 515 547 EGF-LIKE 4.
FT DOMAIN 549 595 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 596 631 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 632 687 VMEC 3.
FT DOMAIN 692 750 VMEC 4.
FT DOMAIN 752 807 VMEC 5.
FT DISULFID 395 407 BY SIMILARITY.
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FT DISULFID 418 432 BY SIMILARITY.
FT DISULFID 438 451 BY SIMILARITY.
FT DISULFID 445 460 BY SIMILARITY.
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FT DISULFID 480 493 BY SIMILARITY.
FT DISULFID 487 502 BY SIMILARITY.
FT DISULFID 504 515 BY SIMILARITY.
FT DISULFID 519 529 BY SIMILARITY.
FT DISULFID 523 535 BY SIMILARITY.
FT DISULFID 537 553 BY SIMILARITY.
FT DISULFID 553 566 BY SIMILARITY.
FT DISULFID 560 575 BY SIMILARITY.
FT DISULFID 577 594 BY SIMILARITY.
FT DISULFID 600 613 BY SIMILARITY.
FT DISULFID 607 622 BY SIMILARITY.
FT DISULFID 624 630 BY SIMILARITY.
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 224 224 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 294 294 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 511 511 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 562 562 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 609 609 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 708 708 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 810 AA; 89212 MW; 46F09CA65AF9AB0B CRC64;

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Query Match Score 30; DB 1; Length 810;
Best Local Similarity 57.1%; Pred. No. 1.7e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 4 NXXCPXC 10
DB 224 NRTCTPC 230

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RESULT 15
NEL2_HUMAN
ID NEL2_HUMAN STANDARD; PRT; 816 AA.
AC 099435;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein kinase C-binding protein NEL2 precursor (NEL-like protein 2)
DE (Nel-related protein 2).
GN NEL2 OR NRP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97131504; PubMed=8975702;
RA Katanabe T.K., Katagiri T., Suzuki M., Shimizu F., Fujiwara T.,
RA Kanemoto N., Nakamura Y., Hirai Y., Mekawa H., Takahashi E.;
RT "Cloning and characterization of two novel human cDNAs (NEL1 and
RT NEL2) encoding proteins with six EGF-like repeats.";
RL Genomics 38:273-276(1996).
RN [2]
RP TSP N-TERMINAL DOMAIN.

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RX MEDLINE=98153258; PubMed=9480764;
RA Beckmann G., Hanke J., Bork P., Reich J.;
RT "Merging extracellular domains: fold prediction for laminin G-like
RT and amino-terminal thrombospondin-like modules based on homology to
RT pentraxins.";
RL J. Mol. Biol. 275:725-730(1998).
CC -1 SUBUNIT: HOMOTRIMER. BINDS TO PKC BETA-1 (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: Secreted (by similarity).
CC -1 SIMILARITY: CONTRAINS 1 TSP N-TERMINAL DOMAIN.
CC -1 SIMILARITY: CONTRAINS 5 VMEC DOMAINS.
CC -1 SIMILARITY: CONTRAINS 6 EGF-LIKE DOMAINS.
-----
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DR EMBL; D83018; BAA11681.1; -
DR HSPB; P00740; 1EDM.
DR Genew; HGNC:7751; NEL2.
DR MIM; 602320; -
DR InterPro; IPR000152; Asx_hydroxyl.
DR InterPro; IPR000561; EGF-like.
DR InterPro; IPR001881; EGF_Ca.
DR InterPro; IPR001791; Laminin_G.
DR InterPro; IPR003129; TSPN.
DR InterPro; IPR001007; VME_C.
DR Pfam; PF00008; EGF; 5.
DR Pfam; PF00093; VME; 3.
DR Pfam; PF02210; TSPN; 1.
DR SMART; SM00179; EGF_CA; 3.
DR SMART; SM00001; EGF_Like; 3.
DR SMART; SM00282; LamG; 1.
DR SMART; SM00210; TSPN; 1.
DR SMART; SM00214; VME; 3.
DR PROSITE; PS00010; ASX_HYDROXYL; 3.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; 4.
DR PROSITE; PS01187; EGF_CA; 3.
DR PROSITE; PS01208; VMEC; 2.
DR Glycoprotein; EGF-like domain; Repeat; Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 816 PROTEIN KINASE C-BINDING PROTEIN NEL2.
FT DOMAIN 30 258 TSP N-TERMINAL.
FT DOMAIN 272 331 VMEC 1.
FT DOMAIN 332 396 VMEC 2.
FT DOMAIN 397 439 EGF-LIKE 1.
FT DOMAIN 440 481 EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 482 522 EGF-LIKE 3.
FT DOMAIN 521 553 EGF-LIKE 4.
FT DOMAIN 555 601 EGF-LIKE 5, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 602 637 EGF-LIKE 6, CALCIUM-BINDING (POTENTIAL).
FT DOMAIN 638 693 VMEC 3.
FT DOMAIN 698 756 VMEC 4.
FT DOMAIN 758 813 VMEC 5.
FT DISULFID 401 413 BY SIMILARITY.
FT DISULFID 407 422 BY SIMILARITY.
FT DISULFID 424 438 BY SIMILARITY.
FT DISULFID 444 457 BY SIMILARITY.
FT DISULFID 451 466 BY SIMILARITY.
FT DISULFID 468 480 BY SIMILARITY.
FT DISULFID 486 499 BY SIMILARITY.
FT DISULFID 493 508 BY SIMILARITY.
FT DISULFID 510 521 BY SIMILARITY.
FT DISULFID 525 535 BY SIMILARITY.
FT DISULFID 529 541 BY SIMILARITY.
FT DISULFID 543 552 BY SIMILARITY.
FT DISULFID 559 566 BY SIMILARITY.
FT DISULFID 583 600 BY SIMILARITY.

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FT	DISULFID	606	619	BY SIMILARITY.
FT	DISULFID	613	628	BY SIMILARITY.
FT	DISULFID	630	636	BY SIMILARITY.
FT	CARBOHYD	53	53	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	225	225	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	293	293	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	298	298	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	517	517	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	615	615	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	635	635	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	816 AA;	91346 MM;	89370B987DC7A324 CRC64;

Query Match 76.98; Score 30; DB 1; Length 816;  
 Best Local Similarity 57.18; Pred. No. 1.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXGCPXC 10  
 DB 225 NRTCPTC 231

Search completed: December 13, 2002, 08:38:37  
 Job time : 2.25153 secs



GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:45 ; Search time 1.91411 Seconds  
(without alignments)  
602.689 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 segs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	79.5	367	2	S48833 cytochrome-c3 hydr
2	31	79.5	367	2	E75133 cytochrome-c3 hydr
3	31	79.5	534	2	T27054 hypothetical prote
4	31	79.5	552	2	H97289 dihydroxy-acid deh
5	30	76.9	113	2	S00118 hypothetical prote
6	30	76.9	117	2	T25411 hypothetical prote
7	30	76.9	117	2	F88765 protein T28C6.8 (1
8	30	76.9	118	2	T27456 hypothetical prote
9	30	76.9	144	2	B82423 thioredoxin 2 VCA0
10	30	76.9	148	2	B72782 hypothetical prote
11	30	76.9	165	2	S52511 hypothetical prote
12	30	76.9	198	2	D82361 conserved hypotet
13	30	76.9	237	1	VCBVMC coat protein - tob
14	30	76.9	280	1	A39131 type IV prepillin p
15	30	76.9	297	2	T28188 hypothetical prote
16	30	76.9	300	2	F90274 pyruvate formate-1
17	30	76.9	335	1	F69052 hypothetical prote
18	30	76.9	343	2	H96703 probable RING zinc
19	30	76.9	348	1	A71012 hypothetical prote
20	30	76.9	349	2	T06680 hypothetical prote
21	30	76.9	352	2	A69103 conserved hypotet
22	30	76.9	362	2	T47910 hypothetical prote
23	30	76.9	407	2	C96657 hypothetical prote
24	30	76.9	481	2	G96835 probable RING zinc
25	30	76.9	495	2	T04466 hypothetical prote
26	30	76.9	544	2	S24915 gene 18 protein -
27	30	76.9	547	2	T37793 probable zinc fing
28	30	76.9	557	2	A48434 variant-specific s
29	30	76.9	612	1	WDBPT5 gene D13 protein -

30	30	76.9	627	1	S27393 splicingmyelin phos
31	30	76.9	634	2	D70331 leucine-trna ligas
32	30	76.9	718	2	T05850 homeobox protein A
33	30	76.9	738	2	E85061 probable homeotic
34	30	76.9	745	2	D96829 homeobox protein (
35	30	76.9	747	2	S71478 homeotic protein A
36	30	76.9	749	2	G86186 homeotic protein,
37	30	76.9	768	2	S71477 hypothetical prote
38	30	76.9	776	2	T20738 homeotic protein,
39	30	76.9	810	2	T10756 hypothetical protei
40	30	76.9	812	2	D96979 leucyl-trna synthet
41	30	76.9	835	2	JP0076 nel protein - chic
42	30	76.9	894	1	SYBYLM leucine-trna ligas
43	30	76.9	894	1	SYBYMX leucine-trna ligas
44	30	76.9	994	1	SYNCLM leucine-trna ligas
45	30	76.9	1083	2	C88854 protein F11A10.3 l

## ALIGNMENTS

RESULT 1  
S48833  
cytochrome-c3 hydrogenase (EC 1.12.2.1) alpha chain - Pyrococcus furiosus  
C:Species: Pyrococcus furiosus  
C:Date: 10-Dec-1994 #sequence\_revision 13-Mar-1997 #text\_change 09-Jun-2000  
C:Accession: S48833  
R:Pedroni, P.  
submitted to the EMBL Data Library, September 1993  
A:Reference number: S48833  
A:Accession: S48833  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <RED>  
A:Cross-references: EMBL:X75255; NID:9562773; PID:9563905  
C:Genetics:  
A:Start codon: GTG  
C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase alpha chain  
C:Keywords: oxidoreductase

Query Match 79.5%; Score 31; DB 2; Length 367;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
DB 240 NTCPTC 246

## RESULT 2

E75133  
cytochrome-c3 hydrogenase (EC 1.12.2.1) beta chain PAB1784 - Pyrococcus abyssi (strai  
C:Species: Pyrococcus abyssi  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Jun-2000  
C:Accession: E75133  
R:anonymous, Genoscope  
submitted to the EMBL Data Library, July 1999  
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome s  
A:Reference number: A75001  
A:Accession: E75133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-367 <RAW>  
A:Cross-references: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CA849782.1; PID:9545  
A:Experimental source: strain Orsay  
C:Genetics:  
A:Gene: PAB1784  
C:Superfamily: Pyrococcus furiosus cytochrome-c3 hydrogenase alpha chain  
C:Keywords: oxidoreductase

Query Match 79.5%; Score 31; DB 2; Length 367;  
Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 240 NTACPTC 246

## RESULT 3

T27054  
hypothetical protein Y49E10.20 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 17-Mar-2000  
C:Accession: T27054  
R:Barlow, K.  
submitted to the EMBL Data Library, August 1997  
A:Reference number: Z20303  
A:Accession: T27054  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-534 <WIL>  
A:Cross-references: EMBL:Z98866; PIDN:CAB11566.1; GSPDB:GN00021; CESP:Y49E10.20  
C:Genetics:  
A:Experimental source: clone Y49E10  
A:Gene: CESP:Y49E10.20  
A:Map position: 3  
A:Introns: 42/3; 105/2; 188/3; 231/3; 359/1; 440/2; 505/3  
C:Superfamily: lysosomal integral membrane protein II

Query Match 79.5%; Score 31; DB 2; Length 534;  
Best Local Similarity 57.1%; Pred. No. 5.1e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 135 NASCPTC 141

## RESULT 4

H97289  
dihydroxy-acid dehydratase [imported] - Clostridium acetobutylicum  
C:Species: Clostridium acetobutylicum  
C>Date: 14-Sep-2001 #sequence\_revision 14-Sep-2001 #text\_change 30-Sep-2001  
C:Accession: H97289  
R:Noelling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.  
J. Bacteriol. 183, 4823-4838, 2001  
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium CLO  
A:Reference number: A96900; MUID:21359325; PMID:21359325  
A:Accession: H97289  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-552 <KUR>  
A:Cross-references: GB:AE001437; PIDN:AAK81107.1; PID:G15026238; GSPDB:GN00168  
C:Experimental source: Clostridium acetobutylicum ATCC824  
C:Genetics:  
A:Gene: CAC3170  
C:Superfamily: dihydroxy-acid dehydratase

Query Match 79.5%; Score 31; DB 2; Length 552;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 182 NTACPTC 188

## RESULT 5

S00118  
hypothetical protein B - Proteus vulgaris  
C:Species: Proteus vulgaris  
C>Date: 31-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 20-Sep-1999  
C:Accession: S00118  
R:Coie, S.T.

Eur. J. Biochem. 167, 481-488, 1987  
A:Title: Nucleotide sequence and comparative analysis of the ftd operon encoding the d-linked ampc cephalosporinase gene.  
A:Reference number: S00107; MUID:88004470; PMID:3308458  
A:Accession: S00118  
A:Molecule type: DNA  
A:Residues: 1-113 <COL>  
A:Cross-references: EMBL:X06151; NID:945907; PIDN:CAA29510.1; PID:945909  
C:Superfamily: hydrogenase accessory protein

Query Match 76.9%; Score 30; DB 2; Length 113;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 86 NACCPAC 92

## RESULT 6

T25411  
hypothetical protein T28C6.8 - Caenorhabditis elegans (fragment)  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T25411  
R:Lloyd, C.  
submitted to the EMBL Data Library, September 1995  
A:Reference number: Z20030  
A:Accession: T25411  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-117 <WIL>  
A:Cross-references: EMBL:Z54238; PIDN:CAA9099.1; GSPDB:GN00022; CESP:T28C6.8  
C:Experimental source: clone T28C6  
C:Genetics:  
A:Gene: CESP:T28C6.8  
A:Map position: 4

Query Match 76.9%; Score 30; DB 2; Length 117;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | |  
Db 8 NLSCPAC 14

## RESULT 7

F88765  
protein T28C6.8 [imported] - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 10-May-2001 #sequence\_revision 10-May-2001 #text\_change 10-May-2001  
C:Accession: F88765  
R:anonymous, The C. elegans Sequencing Consortium.  
Science 282, 2012-2018, 1998  
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating bio  
A:Reference number: A75000; MUID:99069613; PMID:9851916  
A:Note: see websites genome.wustl.edu/gsc/C\_elegans/ and www.sanger.ac.uk/Projects/C-  
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999;  
A:Accession: F88765  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-117 <STO>  
A:Cross-references: GB:chr\_IV; PIDN:CAA90999.1; PID:94038509; GSPDB:GN00022; CESP:T28  
C:Genetics:  
A:Gene: T28C6.8  
A:Map position: 4

Query Match 76.9%; Score 30; DB 2; Length 117;  
Best Local Similarity 57.1%; Pred. No. 2.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10

Db 8 NLSCPAC 14

# RESULT 8

T27456

hypothetical protein Y87G2A.d - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C:Accession: T27456

R:White, S.

submitted to the EMBL Data Library, September 1999

A:Reference number: Z20371

A:Accession: T27456

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-118 <WILD>

A:Cross-references: EMBL:AL110500; NID:e1542314; PIDN:CAB54478.1; CESP:Y87G2A.d

A:Experimental source: clone Y87G2A

C:Genetics:

A:Gene: CESP:Y87G2A.d

A:Introns: 19/3; 52/3

## Query Match

Best Local Similarity 76.9%; Score 30; DB 2; Length 118;  
Pred. No. 3e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10

Db 102 NHSCPAC 108

# RESULT 9

B82423

thioredoxin 2 VCA0752 [imported] - Vibrio cholerae (strain N16961 serogroup O1)

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Feb-2001

C:Accession: B82423

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;

Chardon, D.; Esmolaeva, M.D.; Yamathayan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.

l, R.R.; Mekalanos, J.C.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: B82423

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-144 <HEI>

A:Cross-references: GB:AE004403; GB:AE003853; NID:g9658159; PIDN:AAF96650.1; GSPDB:GN001

A:Experimental source: serogroup O1; strain N16961; biotype El Tor

C:Genetics:

A:Gene: VCA0752

A:Map position: 2

C:Superfamily: thioredoxin; thioredoxin homology

## Query Match

Best Local Similarity 76.9%; Score 30; DB 2; Length 144;  
Pred. No. 3.3e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10

Db 5 NTRCPSC 11

# RESULT 10

B72782

hypothetical protein APE0243 - Aeropyrum pernix (strain K1)

C:Species: Aeropyrum pernix

C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 09-Jun-2000

C:Accession: B72782

R:Kawabayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Halkawa, Y.; Jin-no, K.; Takah

awa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; K

DNA Res. 6, 83-101, 1999

A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aero

A:Reference number: A72450; MUID:99310339; PMID:10382966

A:Accession: B72782

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-148 <KAN>

A:Cross-references: DBJ:AP000058; NID:g5103388; PIDN:BA79156.1; PMID:d1042932; PID:g

A:Experimental source: strain K1

C:Genetics:

A:Gene: APE0243

C:Superfamily: Aeropyrum pernix hypothetical protein APE0243

## Query Match

Best Local Similarity 76.9%; Score 30; DB 2; Length 148;  
Pred. No. 3.4e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10

Db 50 NALCPAC 56

# RESULT 11

S52511

hypothetical protein YD1008w - yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein D2900

C:Species: Saccharomyces cerevisiae

C:Date: 08-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 19-Apr-2002

C:Accession: S52511; S67540

R:Andre, B.; Vissers, S.; Urrestarazu, L.

submitted to the EMBL Data Library, February 1995

A:Description: The sequence of a 42 kb segment located on the left arm of chromosome

A:Reference number: S52492

A:Accession: S52511

A:Molecule type: DNA

A:Residues: 1-165 <AND>

A:Cross-references: EMBL:Z48432; NID:g683669; PIDN:CA88351.1; PID:g683689

A:Experimental source: strain S288C

R:Urrestarazu, L.A.; Andre, B.; Vissers, S.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67535

A:Accession: S67540

A:Molecule type: DNA

A:Residues: 1-165 <URR>

A:Cross-references: EMBL:Z74056; NID:g1430968; PIDN:CA98564.1; PID:e252972; PID:g143

A:Experimental source: strain S288C

C:Genetics:

A:Gene: SGD:APC11

A:Cross-references: SGD:S0002166

A:Map position: 4L

## Query Match

Best Local Similarity 76.9%; Score 30; DB 2; Length 165;  
Pred. No. 3.6e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10

Db 49 NGTSPSC 55

# RESULT 12

D82361

conserved hypothetical protein VC0131 [imported] - Vibrio cholerae (strain N16961 ser

C:Species: Vibrio cholerae

C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 02-Aug-2002

C:Accession: D82361

R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.

Chardon, D.; Esmolaeva, M.D.; Yamathayan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers

l, R.R.; Mekalanos, J.C.; Venter, J.C.; Fraser, C.M.

Nature 406, 477-483, 2000

A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: D82361

A:Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-198 <HEI>  
 A:Cross-references: GB:AE004103; GB:AE003852; NID:9654523; PIDN:AAF93308.1; GSPDB:GN001  
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
 C:Genetics:  
 A:Gene: VC0131  
 A:Map position: 1  
 C:Superfamily: Escherichia coli hypothetical protein b2583

Query Match 76.9%; Score 30; DB 2; Length 198;  
 Best Local Similarity 57.1%; Pred. No. 4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 | | | |  
 Db 2 NAACPDC 8

## RESULT 13

VCBVMC

coat protein - tobacco streak virus (strain WC)

N:Alternate names: P4 protein

C:Species: tobacco streak virus, TSV

A:Note: host Nicotiana glauca x N. clevelandii (tobacco)

C:Date: 28-Aug-1985 #sequence\_revision 28-Aug-1985 #text\_change 23-Jul-1999

C:Accession: A04206

R:Corneilissen, B.J.C.; Janssen, H.; Zuidema, D.; Bol, J.F.

Nucleic Acids Res. 12, 2427-2437, 1984

A:Title: Complete nucleotide sequence of tobacco streak virus RNA 3.

A:Reference number: A93507; MUID:84169544; PMID:6346793

A:Accession: A04206

A:Molecule type: genomic RNA

A:Residues: 1-237 &lt;COR&gt;

A:Cross-references: GB:U00435; NID:962146; PIDN:CAA25133.1; PID:962148

C:Genetics:

A:Map position: segment 3

C:Superfamily: tobacco streak virus coat protein

Query Match 76.9%; Score 30; DB 1; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 | | | |  
 Db 25 NSRCPTC 31

## RESULT 14

A39131

type IV prepilin peptidase (EC 3.4.99.-) pI1D - Pseudomonas aeruginosa

N:Alternate names: inner membrane protein xcpA

C:Species: Pseudomonas aeruginosa

C:Date: 10-Sep-1999 #sequence\_revision 10-Sep-1999 #text\_change 31-Dec-2000

C:Accession: A39131; C35384; D83078

R:Bailey, M.; Bail, G.; Badere, A.; Lazdunski, A.

J. Bacteriol. 173, 479-486, 1991

A:Title: Protein secretion in Pseudomonas aeruginosa: the xcpA gene encodes an integral

A:Reference number: A39131; MUID:91100333; PMID:1698929

A:Accession: A39131

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-290 &lt;BAL&gt;

A:Cross-references: GB:M61096; GB:M38720; NID:9151641; PIDN:AAA26023.1; PID:9151642

R:Nunn, D.; Bergman, S.; Lory, S.

J. Bacteriol. 172, 2911-2919, 1990

A:Title: Products of three accessory genes, pilB, pilC, and pilD, are required for bio

A:Reference number: A35384; MUID:90264276; PMID:1971619

A:Accession: C35384

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-17, 'A', 19-290 &lt;NDN&gt;

A:Cross-references: GB:M32066; NID:9151064; PIDN:AAA25734.1; PID:9151067

A:Note: the authors translated the codon AAC for residue 30 as Ala  
 R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
 Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lartig, K.; L  
 ; Lory, S.; Olson, M.V.  
 Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A:Reference number: A82950; MUID:20437337; PMID:10984043

A:Accession: D83078

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-290 &lt;STO&gt;

A:Cross-references: GB:AE004867; GB:AE004091; NID:9950769; PIDN:AA607916.1; GSPDB:GN

A:Experimental source: strain PA01

C:Genetics:

A:Gene: pilD; xcpA; pilD; PA4528

C:Superfamily: type IV prepilin peptidase

C:Keywords: hydrolase; methyltransferase; S-adenosylmethionine; transmembrane protein

Query Match 76.9%; Score 30; DB 1; Length 290;  
 Best Local Similarity 57.1%; Pred. No. 5e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 | | | |  
 Db 69 NSACPXC 75

## RESULT 15

T28188

hypothetical protein ORF29 - Melanoplus sanguinipes entomopoxvirus (isolate Tuscon)

N:Alternate names: ORF MSV027 tryptophan repeat gene family protein

C:Species: Melanoplus sanguinipes entomopoxvirus

C:Date: 21-Jan-2000 #sequence\_revision 21-Jan-2000 #text\_change 02-Sep-2000

C:Accession: T28188

R:Alonso, C.L.; Fulman, E.R.; Lu, Z.; Oma, E.; Kutish, G.F.; Rock, D.L.

J. Virol. 73, 533-552, 1999

A:Title: The genome of Melanoplus sanguinipes entomopoxvirus.

A:Reference number: 220484; MUID:99102612; PMID:9847359

A:Accession: T28188

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: DNA

A:Residues: 1-297 &lt;AFO&gt;

A:Cross-references: EMBL:AF063866; NID:94049647; PIDN:AA097845.1; PID:94049885

A:Experimental source: isolate Tuscon

C:Genetics:

A:Note: MSV027

C:Superfamily: RING finger homology

F;248-296/Domain: RING finger homology &lt;RRN&gt;

Query Match 76.9%; Score 30; DB 2; Length 297;  
 Best Local Similarity 57.1%; Pred. No. 5.1e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
 | | | |  
 Db 284 NSRCPMC 290

Search completed: December 13, 2002, 08:40:10  
 Job time : 4.91411 secs

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:45 ; Search time 1.91411 Seconds

(without alignments)  
420.734 Million cell updates/sec

Title: US-09-701-080C-1

Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 239201 seqs, 67110966 residues

Total number of hits satisfying chosen parameters: 239201

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

Pending\_Patents\_AA\_New.\*  
1: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/paa/US06\_NEW\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/paa/US07\_NEW\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/paa/US08\_NEW\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/paa/US09\_NEW\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/paa/US10\_NEW\_COMB.pep.\*  
7: /cgn2\_6/ptodata/1/paa/US60\_NEW\_COMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	76.9	84	US-09-513-999C-7264	Sequence 7264, App
2	30	76.9	237	US-09-989-733-295	Sequence 295, App
3	30	76.9	237	US-09-992-643-295	Sequence 295, App
4	30	76.9	237	US-10-125-923A-222	Sequence 222, App
5	30	76.9	237	US-10-205-892-222	Sequence 222, App
6	30	76.9	237	US-10-174-575-222	Sequence 222, App
7	30	76.9	237	US-10-174-575-222	Sequence 222, App
8	30	76.9	237	US-09-724-676-78297	Sequence 78297, A
9	30	76.9	332	US-09-724-676-78297	Sequence 78297, A
10	30	76.9	332	US-09-724-676A-78297	Sequence 78297, A
11	30	76.9	332	US-09-724-676A-78297	Sequence 78297, A
12	30	76.9	332	US-09-724-676-78522	Sequence 78522, A
13	30	76.9	332	US-09-724-676A-78522	Sequence 78522, A
14	30	76.9	332	US-09-724-676A-78522	Sequence 78522, A
15	30	76.9	332	US-09-724-676A-78522	Sequence 78522, A
16	30	76.9	332	US-09-724-676A-78522	Sequence 78522, A
17	30	76.9	332	US-10-286-264-58	Sequence 58, Appl
18	30	76.9	332	US-10-286-264-80	Sequence 80, Appl
19	30	76.9	332	US-10-293-017-14	Sequence 14, Appl
20	30	76.9	332	US-10-293-017-14	Sequence 14, Appl
21	30	76.9	332	US-09-660-568-42	Sequence 42, Appl
22	30	76.9	332	US-10-283-500-11	Sequence 11, Appl
23	30	76.9	332	US-10-283-500-13	Sequence 13, Appl
24	30	76.9	332	US-09-716-536-13	Sequence 13, Appl
25	30	76.9	332	PCT-US02-32727-22116	Sequence 22116, A
26	30	76.9	332	PCT-US02-32727-22116	Sequence 22116, A
				PCT-US02-32727-26222	Sequence 26222, A

27	29	74.4	113	6	US-10-057-498-26222	Sequence 26222, A
28	29	74.4	136	7	US-60-425-113-49	Sequence 49, Appl
29	29	74.4	139	7	US-60-425-113-62	Sequence 62, Appl
30	29	74.4	297	6	US-10-288-160-8	Sequence 8, Appl
31	29	74.4	358	5	US-09-724-676-71193	Sequence 71193, A
32	29	74.4	358	5	US-09-724-676A-71193	Sequence 71193, A
33	29	74.4	358	5	US-10-092-411A-5436	Sequence 5436, Ap
34	29	74.4	452	6	US-10-264-237-2355	Sequence 2355, Ap
35	29	74.4	636	5	US-09-724-676-62863	Sequence 62863, A
36	29	74.4	636	5	US-09-724-676A-62863	Sequence 62863, A
37	29	74.4	642	5	US-09-724-676-62864	Sequence 62864, A
38	29	74.4	649	5	US-09-724-676A-62864	Sequence 62864, A
39	29	74.4	649	5	US-09-724-676-62864	Sequence 62864, A
40	29	74.4	649	5	US-09-724-676A-62862	Sequence 62862, A
41	29	74.4	662	5	US-09-724-676-62865	Sequence 62865, A
42	29	74.4	662	5	US-09-724-676A-62865	Sequence 62865, A
43	29	74.4	723	6	US-10-092-411A-5060	Sequence 5060, Ap
44	29	74.4	813	6	US-10-231-778-2	Sequence 2, Appl
45	28	71.8	12	5	US-09-701-080C-1	Sequence 1, Appl

#### ALIGNMENTS

RESULT 1  
US-09-513-999C-7264  
Sequence 7264, Application US/09513999C  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Duclet, A.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
FILE REFERENCE: 59, US2, REG  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487  
PRIOR FILING DATE: 1999-02-26  
NUMBER OF SEQ ID NOS: 36681  
SOFTWARE: Patent.pm  
SEQ ID NO 7264  
LENGTH: 84  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: UNSURE  
LOCATION: 16  
OTHER INFORMATION: Xaa-Gly or Arg  
US-09-513-999C-7264

Query Match  
Best Local Similarity 76.9%; Score 30; DB 5; Length 84;  
Matches 4; Conservative 0; Mismatches 3; Indels 0;  
DB 20 NSQCPAC 26

RESULT 2  
US-09-989-733-295  
Sequence 295, Application US/09989733  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.

```

: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavain, Ivar J.
: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C68
: CURRENT APPLICATION NUMBER: US/09/989,733
: CURRENT FILING DATE: 2001-11-01
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 295
: LENGTH: 237
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-989-733-295

Query Match
Best Local Similarity 76.9%; Score 30; DB 5; Length 237;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXPCPC 10
      | | |
Db 122 NAECPC 128

RESULT 3
: Sequence 295, Application US/09992643
: GENERAL INFORMATION:
: APPLICANT: Ashkenazi, Avi J.
: APPLICANT: Baker, Kevin P.
: APPLICANT: Bolstein, David
: APPLICANT: Desnoyers, Luc
: APPLICANT: Eaton, Dan L.
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Fong, Sherman
: APPLICANT: Gerber, Hanspeter
: APPLICANT: Geritsen, Mary E.
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Grimaldi, J. Christopher
: APPLICANT: Gurney, Austin L.
: APPLICANT: Kijavain, Ivar J.
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: APPLICANT: Napier, Mary A.
: APPLICANT: Pan, James
: APPLICANT: Paoni, Nicholas F.
: APPLICANT: Roy, Margaret Ann
: APPLICANT: Stewart, Timothy A.
: APPLICANT: Tumas, Daniel
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Williams, P. Mickey
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
: FILE REFERENCE: P2730P1C13
: CURRENT APPLICATION NUMBER: US/09/992,643
: CURRENT FILING DATE: 2001-11-01
: PRIOR APPLICATION NUMBER: 60/049787
: PRIOR FILING DATE: 1997-06-16
: PRIOR APPLICATION NUMBER: 60/062250
: PRIOR FILING DATE: 1997-10-17
: PRIOR APPLICATION NUMBER: 60/065186
: PRIOR FILING DATE: 1997-11-12
: PRIOR APPLICATION NUMBER: 60/065311
: PRIOR FILING DATE: 1997-11-13
: PRIOR APPLICATION NUMBER: 60/066770
: PRIOR FILING DATE: 1997-11-24
: PRIOR APPLICATION NUMBER: 60/075945
: PRIOR FILING DATE: 1998-02-25
: PRIOR APPLICATION NUMBER: 60/078910
: PRIOR FILING DATE: 1998-03-20
: PRIOR APPLICATION NUMBER: 60/083322
: PRIOR FILING DATE: 1998-04-28
: PRIOR APPLICATION NUMBER: 60/084600
: PRIOR FILING DATE: 1998-05-07
: PRIOR APPLICATION NUMBER: 60/087106
: PRIOR FILING DATE: 1998-05-28
: Remaining Prior Application data removed - See File Wrapper or PALM.
: NUMBER OF SEQ ID NOS: 532
: SEQ ID NO 295
: LENGTH: 237
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-992-643-295

Query Match
Best Local Similarity 76.9%; Score 30; DB 5; Length 237;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXPCPC 10
      | | |
Db 122 NAECPC 128

RESULT 4
: Sequence 222, Application US/10125923A
: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin P.
: APPLICANT: Chen, Jian
: APPLICANT: Desnoyers, Luc
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul J.
: APPLICANT: Gurney, Austin L.
: APPLICANT: Pan, James
: APPLICANT: Smith, Victoria
: APPLICANT: Watanabe, Colin K.
: APPLICANT: Wood, William I.
: APPLICANT: Zhang, Zemin
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: FILE REFERENCE: P3430R1C79
: CURRENT APPLICATION NUMBER: US/10/125,923A
: CURRENT FILING DATE: 2002-01-15
: PRIOR APPLICATION NUMBER: 10/052586
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; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-125-923A-222
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Query Match          76.9%; Score 30; DB 6; Length 237;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 4 NXXCPXC 10
Db 122 NAECPC 128
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RESULT 5
US-10-205-892-222
; Sequence 222, Application US/10205892
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C517
; CURRENT APPLICATION NUMBER: US/10/205,892
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
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; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-205-892-222
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Query Match          76.9%; Score 30; DB 6; Length 237;
Best Local Similarity 57.1%; Pred. No. 3e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 4 NXXCPXC 10
Db 122 NAECPC 128
```

```

RESULT 6
US-10-174-575-222
; Sequence 222, Application US/10174575
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C35
; CURRENT APPLICATION NUMBER: US/10/174,575
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 222
; LENGTH: 237
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-174-575-222
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Db 122 NAECPAC 128

## RESULT 7

US-10-174-575A-222  
; Sequence 222, Application US/10174575A  
; GENERAL INFORMATION:  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Chen, Jian  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Pan, James  
; APPLICANT: Smith, Victoria  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC  
; FILE REFERENCE: P3430R1C35  
; CURRENT APPLICATION NUMBER: US/10/174,575A  
; CURRENT FILING DATE: 2002-06-18  
; PRIOR APPLICATION NUMBER: 10/052586  
; PRIOR FILING DATE: 2002-01-15  
; PRIOR APPLICATION NUMBER: 60/059263  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/059266  
; PRIOR FILING DATE: 1997-09-18  
; PRIOR APPLICATION NUMBER: 60/062250  
; PRIOR FILING DATE: 1997-10-17  
; PRIOR APPLICATION NUMBER: 60/063120  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063121  
; PRIOR FILING DATE: 1997-10-24  
; PRIOR APPLICATION NUMBER: 60/063486  
; PRIOR FILING DATE: 1997-10-21  
; PRIOR APPLICATION NUMBER: 60/063540  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063541  
; PRIOR FILING DATE: 1997-10-28  
; PRIOR APPLICATION NUMBER: 60/063544  
; PRIOR FILING DATE: 1997-10-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 612  
; SEQ ID NO 232  
; LENGTH: 237  
; TYPE: PRT  
; ORGANISM: Homo Sapien  
US-10-174-575A-222

Query Match 76.9%; Score 30; DB 6; Length 237;  
Best Local Similarity 57.1%; Pred. No. 3e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 122 NAECPAC 128

## RESULT 8

US-09-724-676-78297  
; Sequence 78297, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78297

; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-78297

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPCT 231

## RESULT 9

US-09-724-676-78298  
; Sequence 78298, Application US/09724676  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78298  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676-78298

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPCT 231

## RESULT 10

US-09-724-676A-78297  
; Sequence 78297, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen  
; CURRENT APPLICATION NUMBER: US/09/724,676A  
; CURRENT FILING DATE: 2000-11-28  
; NUMBER OF SEQ ID NOS: 97222  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 78297  
; LENGTH: 332  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-724-676A-78297

Query Match 76.9%; Score 30; DB 5; Length 332;  
Best Local Similarity 57.1%; Pred. No. 3.6e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
Db 225 NRTCPCT 231

## RESULT 11

US-09-724-676A-78298  
; Sequence 78298, Application US/09724676A  
; GENERAL INFORMATION:  
; APPLICANT: Compugen LTD  
; TITLE OF INVENTION: Variants of alternative splicing  
; FILE REFERENCE: 129181.4 Compugen



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; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78298
; LENGTH: 332
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78298
```

```
Query Match          76.9%; Score 30; DB 5; Length 332;
Best Local Similarity 57.1%; Pred. No. 3.6e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 4 NXXCPXC 10
DB 225 NHTCPTC 231
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```
RESULT 12
US-09-724-676-78522
; Sequence 78522, Application US/09724676
; GENERAL INFORMATION:
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; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78522
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78522
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Query Match          76.9%; Score 30; DB 5; Length 550;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 4 NXXCPXC 10
DB 224 NHTCPTC 230
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```
RESULT 13
US-09-724-676A-78522
; Sequence 78522, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78522
; LENGTH: 550
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78522
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```
Query Match          76.9%; Score 30; DB 5; Length 550;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 4 NXXCPXC 10
DB 224 NHTCPTC 230
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```
RESULT 14
US-09-724-676-78521
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; Sequence 78521, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-78521
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Query Match          76.9%; Score 30; DB 5; Length 555;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
QY 4 NXXCPXC 10
DB 224 NHTCPTC 230
```

```
RESULT 15
US-09-724-676A-78521
; Sequence 78521, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 78521
; LENGTH: 555
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-78521
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Query Match          76.9%; Score 30; DB 5; Length 555;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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QY 4 NXXCPXC 10
DB 224 NHTCPTC 230
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Job time: 1.91411 secs
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CLANK (USPTO)

GenCore version 5.1.3  
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:37:10 ; Search time 20.0982 Seconds  
(without alignments)  
384.951 Million cell updates/sec

Title: US-09-701-080C-1

Perfect score: 39

Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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27: /cgn2\_6/ptodata/1/paa/US60\_COMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	31	79.5	79	21	US-09-733-089-23902
2	31	79.5	79	22	US-09-816-660-23902
3	31	79.5	82	21	US-09-733-089-20004
4	31	79.5	82	22	US-09-816-660-20004
5	31	79.5	243	25	US-10-155-881-9389
6	31	79.5	339	25	US-10-155-881-29457

7	31	79.5	367	21	US-09-791-537-12171	Sequence 12171, A
8	31	79.5	367	21	US-09-791-537-15887	Sequence 15887, A
9	31	79.5	534	27	US-60-360-039-5906	Sequence 5906, Ap
10	31	79.5	635	19	US-09-540-236-2296	Sequence 2296, Ap
11	31	79.5	635	27	US-60-128-476-3650	Sequence 3650, Ap
12	30	76.9	19	1	PCT-US94-07194-3	Sequence 3, Appl1
13	30	76.9	61	26	US-10-219-999-51491	Sequence 51491, A
14	30	76.9	61	27	US-60-312-544-7377	Sequence 7377, A
15	30	76.9	73	17	US-09-330-781-260	Sequence 260, App
16	30	76.9	73	22	US-09-828-769-260	Sequence 260, App
17	30	76.9	75	21	US-09-708-427-58792	Sequence 58792, A
18	30	76.9	78	20	US-09-617-681A-5073	Sequence 5073, Ap
19	30	76.9	87	20	US-09-617-682A-925	Sequence 925, App
20	30	76.9	87	25	US-10-155-881-22445	Sequence 22445, A
21	30	76.9	88	21	US-09-733-089-15530	Sequence 15530, A
22	30	76.9	88	22	US-09-816-660-15530	Sequence 15530, A
23	30	76.9	93	21	US-09-708-427-58791	Sequence 58791, A
24	30	76.9	96	22	US-09-733-089-5237	Sequence 5237, Ap
25	30	76.9	96	22	US-09-816-660-5237	Sequence 5237, Ap
26	30	76.9	100	21	US-09-708-427-58790	Sequence 58790, A
27	30	76.9	100	25	US-10-155-881-34015	Sequence 34015, A
28	30	76.9	100	27	US-60-312-544-6413	Sequence 6413, Ap
29	30	76.9	100	27	US-60-324-109-20832	Sequence 20832, A
30	30	76.9	101	23	US-09-902-540-16156	Sequence 16156, A
31	30	76.9	104	20	US-09-617-681A-5072	Sequence 5072, Ap
32	30	76.9	104	21	US-09-733-089-5145	Sequence 5145, Ap
33	30	76.9	104	22	US-09-816-660-5145	Sequence 5145, Ap
34	30	76.9	104	25	US-10-155-881-22620	Sequence 22620, Ap
35	30	76.9	110	25	US-10-155-881-34028	Sequence 34028, A
36	30	76.9	113	20	US-09-617-682A-924	Sequence 924, App
37	30	76.9	115	25	US-10-155-881-44013	Sequence 44013, A
38	30	76.9	115	27	US-60-312-544-6368	Sequence 6368, Ap
39	30	76.9	116	19	US-09-543-681A-6234	Sequence 6234, Ap
40	30	76.9	118	1	PCT-US01-04098A-3697	Sequence 3697, Ap
41	30	76.9	119	21	US-09-708-427-58791	Sequence 58791, A
42	30	76.9	120	21	US-09-733-089-15442	Sequence 15442, A
43	30	76.9	120	22	US-09-816-660-15442	Sequence 15442, A
44	30	76.9	122	25	US-10-155-881-33987	Sequence 33987, A
45	30	76.9	122	27	US-60-312-544-5588	Sequence 5588, Ap

#### ALIGNMENTS

RESULT 1

US-09-733-089-23902

; Sequence 23902, Application US/09733089

; GENERAL INFORMATION:

; APPLICANT: Dotson, Stanton B.

; APPLICANT: Kovacic, David K.

; APPLICANT: Liu, Jingdong

; APPLICANT: Lutfiyya, Linda L.

; APPLICANT: McIninch, James

; APPLICANT: Wu, Wei

; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With

; FILE REFERENCE: 38-21(15300)D

; CURRENT APPLICATION NUMBER: US/09/733,089

; PRIOR FILING DATE: 2000-12-11

; PRIOR APPLICATION NUMBER: US 09/474,435

; PRIOR FILING DATE: 1999-12-28

; PRIOR APPLICATION NUMBER: US 09/654,617

; PRIOR FILING DATE: 2000-09-05

; PRIOR APPLICATION NUMBER: US 09/620,392

; PRIOR FILING DATE: 2000-07-19

; NUMBER OF SEQ ID NOS: 24143

; SEQ ID NO 23902

; LENGTH: 79

; TYPE: PRT

; ORGANISM: Oryza sativa

US-09-733-089-23902

Query Match 79.5%; Score 31; DB 21; Length 79;

Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
| | | |  
Db 31 NSSCPC 37

## RESULT 2

US-09-816-660-23902  
; Sequence 23902, Application US/09816660  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/816,660  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: ) US 09/684,016  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 23902  
; LENGTH: 79  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-816-660-23902

Query Match 79.5%; Score 31; DB 22; Length 79;  
Best Local Similarity 57.1%; Pred. No. 1.9e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
| | | |  
Db 31 NSSCPC 37

## RESULT 3

US-09-733-089-20004  
; Sequence 20004, Application US/09733089  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 20004  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Zea mays

; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-733-089-20004

Query Match 79.5%; Score 31; DB 21; Length 82;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
| | | |  
Db 20 NSSCPC 26

## RESULT 4

US-09-816-660-20004  
; Sequence 20004, Application US/09816660  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; APPLICANT: Wu, Wei  
; TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With  
; FILE REFERENCE: 38-21(15300)D  
; CURRENT APPLICATION NUMBER: US/09/816,660  
; PRIOR FILING DATE: 2001-03-26  
; PRIOR APPLICATION NUMBER: US 09/474,435  
; PRIOR FILING DATE: 1999-12-28  
; PRIOR APPLICATION NUMBER: US 09/654,617  
; PRIOR FILING DATE: 2000-09-05  
; PRIOR APPLICATION NUMBER: US 09/733,089  
; PRIOR FILING DATE: 2000-12-11  
; PRIOR APPLICATION NUMBER: ) US 09/684,016  
; PRIOR FILING DATE: 2000-10-10  
; PRIOR APPLICATION NUMBER: US 09/620,392  
; PRIOR FILING DATE: 2000-07-19  
; NUMBER OF SEQ ID NOS: 24143  
; SEQ ID NO 20004  
; LENGTH: 82  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-09-816-660-20004

Query Match 79.5%; Score 31; DB 22; Length 82;  
Best Local Similarity 57.1%; Pred. No. 2e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPC 10  
| | | |  
Db 20 NSSCPC 26

## RESULT 5

US-10-155-881-9389  
; Sequence 9389, Application US/10155881  
; GENERAL INFORMATION:  
; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovall, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(15300)J  
; CURRENT APPLICATION NUMBER: US/10/155,881  
; PRIOR FILING DATE: 2002-05-22  
; NUMBER OF SEQ ID NOS: 37595  
; SEQ ID NO 9389  
; LENGTH: 243  
; TYPE: PRT  
; ORGANISM: Zea mays

US-10-155-881-9389

Query Match 79.5%; Score 31; DB 25; Length 243;  
Best Local Similarity 57.1%; Pred. No. 4.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 23 NASCPSC 29

RESULT 6  
US-10-155-881-29457

; Sequence 29457, Application US/10155881  
; GENERAL INFORMATION:

; APPLICANT: Dotson, Stanton B.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jingdong  
; APPLICANT: Lutfiyya, Linda L.  
; APPLICANT: McIninch, James  
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND OTHER MOLECULES ASSOCIATED WITH  
; FILE REFERENCE: 38-21(15300)J  
; CURRENT APPLICATION NUMBER: US/10/155,881  
; CURRENT FILING DATE: 2002-05-22  
; NUMBER OF SEQ ID NOS: 37595  
; SEQ ID NO 29457  
; LENGTH: 339  
; TYPE: PRT  
; ORGANISM: Oryza sativa  
US-10-155-881-29457

Query Match 79.5%; Score 31; DB 25; Length 339;  
Best Local Similarity 57.1%; Pred. No. 5.1e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 277 NSSCPSC 283

RESULT 7  
US-09-791-537-12171

; Sequence 12171, Application US/09791537  
; GENERAL INFORMATION:  
; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY MEMB  
; TITLE OF INVENTION: METHODS OF USE THEREOF  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 12171  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Pyrococcus abyssi  
US-09-791-537-12171

Query Match 79.5%; Score 31; DB 21; Length 367;  
Best Local Similarity 57.1%; Pred. No. 5.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 240 NTTCPTC 246

RESULT 8  
US-09-791-537-15887  
; Sequence 15887, Application US/09791537

; GENERAL INFORMATION:

; APPLICANT: Bionomix, Inc.  
; APPLICANT: Debe, Derek  
; APPLICANT: Danzer, Joseph  
; TITLE OF INVENTION: THREE DIMENSIONAL STRUCTURES OF PROTEIN FAMILIES AND FAMILY ME  
; FILE REFERENCE: 261/210  
; CURRENT APPLICATION NUMBER: US/09/791,537  
; CURRENT FILING DATE: 2001-02-22  
; NUMBER OF SEQ ID NOS: 153055  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 15887  
; LENGTH: 367  
; TYPE: PRT  
; ORGANISM: Pyrococcus furiosus  
US-09-791-537-15887

Query Match 79.5%; Score 31; DB 21; Length 367;  
Best Local Similarity 57.1%; Pred. No. 5.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 240 NTTCPTC 246

RESULT 9  
US-60-360-039-5906

; Sequence 5906, Application US/60360039  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Chen, Xianfeng  
; APPLICANT: Goldman, Barry S.  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Slater, Steven C.  
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF  
; FILE REFERENCE: 38-10(52052)A  
; CURRENT APPLICATION NUMBER: US/60/360,039  
; CURRENT FILING DATE: 2002-02-21  
; NUMBER OF SEQ ID NOS: 47374  
; SEQ ID NO 5906  
; LENGTH: 534  
; TYPE: PRT  
; ORGANISM: Caenorhabditis elegans  
US-60-360-039-5906

Query Match 79.5%; Score 31; DB 27; Length 534;  
Best Local Similarity 57.1%; Pred. No. 6.8e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
| | | |  
Db 135 NASCPSC 141

RESULT 10  
US-09-540-236-2296

; Sequence 2296, Application US/09540236  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA CA  
; FILE REFERENCE: 2709.2005-001  
; CURRENT APPLICATION NUMBER: US/09/540,236  
; CURRENT FILING DATE: 2000-04-04  
; NUMBER OF SEQ ID NOS: 3840  
; SEQ ID NO 2296  
; LENGTH: 635  
; TYPE: PRT  
; ORGANISM: M. catarrhalis  
US-09-540-236-2296

Query Match 79.5%; Score 31; DB 19; Length 635;  
Best Local Similarity 57.1%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 206 NSACPTC 212

RESULT 11  
US-60-128-476-3650  
; Sequence 3650, Application US/60128476  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Bretton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO MORAXELLA  
; FILE REFERENCE: 107196.139  
; CURRENT APPLICATION NUMBER: US/60/128,476  
; CURRENT FILING DATE: 1999-04-09  
; NUMBER OF SEQ ID NOS: 5002  
; SEQ ID NO 3650  
; LENGTH: 635  
; TYPE: PRT  
; ORGANISM: Moraxella catarrhalis  
US-60-128-476-3650

Query Match 79.5%; Score 31; DB 27; Length 635;  
Best Local Similarity 57.1%; Pred. No. 7.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 206 NSACPTC 212

RESULT 12  
PCT-US94-07194-3  
; Sequence 3, Application PC/TUS9407194  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: CONOTOXINS I  
; NUMBER OF SEQUENCES: 13  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent in Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/07194  
; FILING DATE: 27-JUN-1994  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/084,848  
; FILING DATE: June 29, 1993  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
PCT-US94-07194-3

Query Match 76.9%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 1.1e+03;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 6 NAACPXC 12

RESULT 13  
US-10-219-999-51491

; Sequence 51491, Application US/10219999  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; APPLICANT: Stein, Joshua  
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-10(52726)C  
; CURRENT APPLICATION NUMBER: US/10/219,999  
; CURRENT FILING DATE: 2002-08-15  
; PRIOR APPLICATION NUMBER: US 60/324,109  
; PRIOR FILING DATE: 2001-09-21  
; PRIOR APPLICATION NUMBER: US 60/312,544  
; PRIOR FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 63520  
; SEQ ID NO 51491  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Zea mays  
US-10-219-999-51491

Query Match 76.9%; Score 30; DB 26; Length 61;  
Best Local Similarity 57.1%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 46 NATCPLC 52

RESULT 14  
US-60-312-544-7377  
; Sequence 7377, Application US/60312544  
; GENERAL INFORMATION:  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Edgerton, Michael D  
; APPLICANT: Hinkle, Gregory J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Liu, Jindong  
; APPLICANT: Stein, Joshua  
; TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT  
; FILE REFERENCE: 38-10(52726)A  
; CURRENT APPLICATION NUMBER: US/60/312,544  
; CURRENT FILING DATE: 2001-08-15  
; NUMBER OF SEQ ID NOS: 10730  
; SEQ ID NO 7377  
; LENGTH: 61  
; TYPE: PRT  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: 701125331\_FLI  
US-60-312-544-7377

Query Match 76.9%; Score 30; DB 27; Length 61;  
Best Local Similarity 57.1%; Pred. No. 2.3e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPCX 10  
| | | |  
Db 36 NSTCPLC 42

RESULT 15  
US-09-330-781-260  
; Sequence 260, Application US/09330781  
; GENERAL INFORMATION:  
; APPLICANT: Geating, David P.  
; APPLICANT: Robison, Keith E.  
; APPLICANT: Holtzman, Douglas A.  
; TITLE OF INVENTION: Nucleic Acid Molecules Derived from a  
; TITLE OF INVENTION: Human Prostate Stromal Cell Library

FILE REFERENCE: MLN98-26pA  
CURRENT APPLICATION NUMBER: US/09/330,781  
CURRENT FILING DATE: 1999-06-11  
PRIOR APPLICATION NUMBER: 60/090,179  
PRIOR FILING DATE: 1998-06-22  
NUMBER OF SEQ ID NOS: 490  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO: 260  
LENGTH: 73  
TYPE: PRF  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: SIGNAL  
LOCATION: (1)...(23)  
US-09-330-781-260

Query Match 76.9%; Score 30; DB 17; Length 73;  
Best Local Similarity 57.1%; Pred. No. 2.6e+03;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPYC 10  
DB 49 NSOCPAC 55

Search completed: December 13, 2002, 08:44:49  
Job time: 22.0982 secs

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GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:39:46 ; Search time 1.17791 Seconds  
(without alignments)  
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Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXNXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

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Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

Published\_Applications\_AA.\*  
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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB.pep.\*  
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12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB.pep.\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	76.9	147	10	US-09-764-864-1289
2	30	76.9	199	10	US-09-764-864-1291
3	30	76.9	201	10	US-09-764-864-836
4	30	76.9	237	9	US-09-992-598-295
5	30	76.9	237	9	US-09-982-293A-295
6	30	76.9	237	10	US-09-989-722-295
7	30	76.9	237	10	US-09-989-723-295
8	30	76.9	237	10	US-09-989-279-295
9	30	76.9	237	10	US-09-989-727-295
10	30	76.9	237	10	US-09-989-731-295
11	30	76.9	237	10	US-09-989-732-295
12	30	76.9	237	10	US-09-991-073-295
13	30	76.9	237	10	US-09-990-442-295
14	30	76.9	237	10	US-09-991-163-295
15	30	76.9	237	10	US-09-993-604-295
16	30	76.9	237	10	US-09-990-456-295
17	30	76.9	237	10	US-09-989-721-295
18	30	76.9	237	12	US-10-052-586-222
19	30	76.9	266	10	US-09-764-864-834

20	30	76.9	718	10	US-09-823-635-2	Sequence 2, Appli
21	30	76.9	810	10	US-09-976-165-34	Sequence 34, Appl
22	30	76.9	816	10	US-09-976-165-37	Sequence 37, Appl
23	29	74.4	149	10	US-09-804-969-8	Sequence 8, Appli
24	29	74.4	164	10	US-09-925-301-1278	Sequence 1278, Ap
25	29	74.4	239	10	US-09-804-969-2	Sequence 2, Appli
26	29	74.4	239	10	US-09-804-969-10	Sequence 10, Appli
27	29	74.4	261	10	US-09-804-969-12	Sequence 12, Appl
28	29	74.4	329	10	US-09-804-969-4	Sequence 4, Appli
29	29	74.4	336	9	US-09-991-888-2	Sequence 2, Appli
30	29	74.4	351	10	US-09-804-969-6	Sequence 6, Appli
31	29	74.4	580	10	US-09-925-301-943	Sequence 943, App
32	29	74.4	642	9	US-10-145-949A-8	Sequence 8, Appli
33	29	74.4	647	9	US-10-145-949A-6	Sequence 6, Appli
34	29	74.4	679	9	US-10-145-949A-4	Sequence 4, Appli
35	29	74.4	684	9	US-10-145-949A-2	Sequence 2, Appli
36	29	74.4	710	10	US-09-815-242-5367	Sequence 5367, Ap
37	29	74.4	711	10	US-09-815-242-12190	Sequence 12190, A
38	29	74.4	940	10	US-09-815-242-10447	Sequence 10447, A
39	29	74.4	943	10	US-09-815-242-10994	Sequence 10994, A
40	29	74.4	1065	10	US-09-900-237-33	Sequence 33, Appl
41	28	71.8	106	10	US-09-764-864-1478	Sequence 1478, Ap
42	28	71.8	113	10	US-09-826-312-8	Sequence 8, Appli
43	28	71.8	118	10	US-09-764-864-826	Sequence 826, App
44	28	71.8	131	10	US-09-764-864-1285	Sequence 1285, Ap
45	28	71.8	404	10	US-09-764-864-1055	Sequence 1055, Ap

#### ALIGNMENTS

RESULT 1  
US-09-764-864-1289  
; Sequence 1289, Application US/09764864  
; Patent No. US20020132753A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PT223  
; CURRENT APPLICATION NUMBER: US/09/764, 864  
; PRIORITY FILING DATE: 2001-01-17  
; Prior application data removed - consult PALM or file wrapper  
; NUMBER OF SEQ ID NOS: 1792  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1289  
; LENGTH: 147  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SITE  
; LOCATION: (95)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (128)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
; NAME/KEY: SITE  
; LOCATION: (147)  
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-764-864-1289

Query Match  
Best local Similarity 76.9%; Score 30; DB 10; Length 147;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

DB 27 NSCPCAC 33

QY 4 NXXCPXC 10

RESULT 2  
US-09-764-864-1291  
; Sequence 1291, Application US/09764864  
; Patent No. US20020132753A1

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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; PRIOR APPLICATION DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1291
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (187)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-864-1291

Query Match
Best Local Similarity 76.9%; Score 30; DB 10; Length 199;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXCPXC 10
Db 179 NSTCPIC 185

RESULT 3
US-09-764-864-836
; Sequence 836, Application US/09764864
; Patent No. US20020132753A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT223
; CURRENT APPLICATION NUMBER: US/09/764,864
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PAM or file wrapper
; NUMBER OF SEQ ID NOS: 1792
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 836
; LENGTH: 201
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-864-836

Query Match
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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Db 181 NSTCPIC 187

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US-09-992-598-295
; Sequence 295, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
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; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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; PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-07  
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PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 9; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
Db 122 NAECPAC 128

RESULT 5  
US-09-989-293A-295  
Sequence 295, Application US/09989293A  
Patent No. US20020177164A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Bostein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerritsen, Mary E.  
APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kljavin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
APPLICANT: Paoni, Nicholas F.  
APPLICANT: Roy, Margaret Ann  
APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
FILE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730P1C66  
CURRENT APPLICATION NUMBER: US/09/989,293A  
PRIOR FILING DATE: 2001-11-20  
PRIOR APPLICATION NUMBER: 60/049787  
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PRIOR APPLICATION NUMBER: 60/090557  
PRIOR FILING DATE: 1998-06-24  
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;; PRIOR APPLICATION NUMBER: 60/090678  
;; PRIOR FILING DATE: 1998-06-25  
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;; PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 9; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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Db 122 NACCPAC 128

RESULT 6  
US-09-989-722-295  
; Sequence 295, Application US/09989722  
; Patent No. US2002072067A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertschen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Grimaldi, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kljavin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; TITLE OF INVENTION: Acids Encoding the Same

;; FILE REFERENCE: P2730PIC63  
;; CURRENT APPLICATION NUMBER: US/09/989,722  
;; CURRENT FILING DATE: 2001-11-19  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPC 10  
I I I  
Db 122 NAECPAC 128

RESULT 7  
US-09-989-723-295  
; Sequence 295, Application US/09989723  
; Patent No. US20020072092A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Bolstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Geriltsen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PLC62  
; CURRENT APPLICATION NUMBER: US/09/989,723  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/049787  
; PRIOR FILING DATE: 1997-06-16  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
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QY 4 NXXCPXC 10  
 Db 122 NAECPAC 128

RESULT 9  
 US-09-989-727-295  
 Sequence 295, Application US/09989727  
 Patent No. US20020072497A1  
 GENERAL INFORMATION:  
 APPLICANT: Ashkenazi, Avi J.  
 APPLICANT: Baker, Kevin P.  
 APPLICANT: Botstein, David  
 APPLICANT: Desnoyers, Luc  
 APPLICANT: Eaton, Dan L.  
 APPLICANT: Ferrara, Napoleone  
 APPLICANT: Fong, Sherman  
 APPLICANT: Geider, Hanspeter  
 APPLICANT: Gerritsen, Mary E.  
 APPLICANT: Goddard, Audrey  
 APPLICANT: Godowski, Paul J.  
 APPLICANT: Grimaldi, J. Christopher  
 APPLICANT: Gurney, Austin L.  
 APPLICANT: Kljavin, Ivar J.  
 APPLICANT: Napier, Mary A.  
 APPLICANT: Pan, James  
 APPLICANT: Paoni, Nicholas F.  
 APPLICANT: Roy, Margaret Ann  
 APPLICANT: Stewart, Timothy A.  
 APPLICANT: Tumas, Daniel  
 APPLICANT: Watanabe, Colin K.  
 APPLICANT: Williams, P. Mickey  
 APPLICANT: Wood, William I.  
 APPLICANT: Zhang, Zemin  
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
 FILE REFERENCE: P2730PC65  
 CURRENT FILING DATE: 2001-11-19  
 PRIOR APPLICATION NUMBER: 60/049787  
 PRIOR FILING DATE: 1997-06-16  
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75	PRIOR FILING DATE: 1998-07-07

;; PRIOR APPLICATION NUMBER: 60/091982  
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;; PRIOR APPLICATION NUMBER: 60/092182  
;; PRIOR FILING DATE: 1998-07-09

Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10

DB 122 NAECPAC 128

RESULT 10

US-09-989-731-295  
; Sequence 295, Application US/09989731  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gurney, Austin L.  
; APPLICANT: Kjaer, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Paoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Watanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730P1C70  
; CURRENT FILING DATE: 2001-11-20  
; PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 76.98; Score 30; DB 10; Length 237;  
Best Local Similarity 57.18; Pred. No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
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RESULT 11  
US-09-989-732-295  
; Sequence 295, Application US/09989732  
; Patent No. US20020123463A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
; APPLICANT: Gertlisen, Mary E.  
; APPLICANT: Goddard, Audrey  
; APPLICANT: Godowski, Paul J.  
; APPLICANT: Grimaldi, J. Christopher  
; APPLICANT: Gunney, Austin L.  
; APPLICANT: Kijavlin, Ivar J.  
; APPLICANT: Napier, Mary A.  
; APPLICANT: Pan, James  
; APPLICANT: Peoni, Nicholas F.  
; APPLICANT: Roy, Margaret Ann  
; APPLICANT: Stewart, Timothy A.  
; APPLICANT: Tumas, Daniel  
; APPLICANT: Matanabe, Colin K.  
; APPLICANT: Williams, P. Mickey  
; APPLICANT: Wood, William I.  
; APPLICANT: Zhang, Zemin  
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
; FILE REFERENCE: P2730PIC57  
; CURRENT APPLICATION NUMBER: US/09/989,732  
; CURRENT FILING DATE: 2001-11-19  
;; PRIOR APPLICATION NUMBER: 60/049787  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
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RESULT 12  
US-09-991-073-295  
Sequence 295, Application US/09991073  
Patent No. US2002012756A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
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APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same  
FILE REFERENCE: P2730PIC15  
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Query Match 76.9%; Score 30; DB 10; Length 237;  
Best Local Similarity 57.1%; Pred. No. 1.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
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Db 122 NACPCAC 128

RESULT 13  
US-09-990-442-295  
; Sequence 295; Application US/09990442  
; Patent No. US20020132252A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.

;; APPLICANT: Botstein, David  
;; APPLICANT: Desnoyers, Luc  
;; APPLICANT: Eaton, Dan L.  
;; APPLICANT: Ferrara, Napoleone  
;; APPLICANT: Fong, Sherman  
;; APPLICANT: Gerber, Hanspeter  
;; APPLICANT: Gerritsen, Mary E.  
;; APPLICANT: Goddard, Audrey  
;; APPLICANT: Godowski, Paul J.  
;; APPLICANT: Grimaldi, J. Christopher  
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;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
;; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
;; FILE REFERENCE: P2730P18  
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;; CURRENT APPLICATION NUMBER: US/09/990,442  
;; PRIOR FILING DATE: 2001-11-14  
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Query Match 76.9% Score 30; DB 10; Length 237;  
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Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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RESULT 14  
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Sequence 295, Application US/09991163  
Patent No. US20020132253A1  
GENERAL INFORMATION:  
APPLICANT: Ashkenazi, Avi J.  
APPLICANT: Baker, Kevin P.  
APPLICANT: Botstein, David  
APPLICANT: Desnoyers, Luc  
APPLICANT: Eaton, Dan L.  
APPLICANT: Ferrara, Napoleone  
APPLICANT: Fong, Sherman  
APPLICANT: Gerber, Hanspeter  
APPLICANT: Gerlitsen, Mary E.



APPLICANT: Goddard, Audrey  
APPLICANT: Godowski, Paul J.  
APPLICANT: Grimaldi, J. Christopher  
APPLICANT: Gurney, Austin L.  
APPLICANT: Kijavlin, Ivar J.  
APPLICANT: Napier, Mary A.  
APPLICANT: Pan, James  
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APPLICANT: Stewart, Timothy A.  
APPLICANT: Tumas, Daniel  
APPLICANT: Watanabe, Colin K.  
APPLICANT: Williams, P. Mickey  
APPLICANT: Wood, William I.  
APPLICANT: Zhang, Zemin  
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic  
TITLE OF INVENTION: Acids Encoding the Same  
FILE REFERENCE: P2730PIC17  
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; Sequence 295, Application US/09993604  
; Patent No. US20020137075A1  
; GENERAL INFORMATION:  
; APPLICANT: Ashkenazi, Avi J.  
; APPLICANT: Baker, Kevin P.  
; APPLICANT: Botstein, David  
; APPLICANT: Desnoyers, Luc  
; APPLICANT: Eaton, Dan L.  
; APPLICANT: Ferrara, Napoleone  
; APPLICANT: Fong, Sherman  
; APPLICANT: Gerber, Hanspeter  
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; APPLICANT: Goddard, Audrey  
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; APPLICANT: Pan, James

;; APPLICANT: Paoni, Nicholas F.  
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;; APPLICANT: Tumas, Daniel  
;; APPLICANT: Watanabe, Colin K.  
;; APPLICANT: Williams, P. Mickey  
;; APPLICANT: Wood, William I.  
;; APPLICANT: Zhang, Zemin  
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;; TITLE OF INVENTION: Acids Encoding the Same  
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## Query Match

76.9%; Score 30; DB 10; Length 237;

Best Local Similarity 57.1%; Pred No. 1.5e+02;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:38:20 ; Search time 1.69325 Seconds  
(without alignments)  
208.519 Million cell updates/sec

Title: US-09-701-080C-1  
Perfect score: 39  
Sequence: 1 XXXXXXCPXCXX 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-Processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*  
1: /cgn2\_6/ptodata/1/1aa/5A.COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B.COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A.COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B.COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/PCROS.COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	76.9	19	1	US-08-084-848A-3
2	30	76.9	19	1	US-08-458-499-3
3	30	76.9	237	4	US-09-227-357-154
4	30	76.9	718	2	US-08-560-398-12
5	30	76.9	768	2	US-08-560-398-2
6	30	76.9	810	2	US-08-820-170A-34
7	30	76.9	810	3	US-09-055-699-34
8	30	76.9	810	4	US-09-273-565-34
9	30	76.9	810	4	US-09-565-538-34
10	30	76.9	810	4	US-09-661-468-34
11	30	76.9	816	2	US-08-820-170A-37
12	30	76.9	816	3	US-09-055-699-37
13	30	76.9	816	3	US-09-273-565-37
14	30	76.9	816	4	US-09-565-538-37
15	30	76.9	816	4	US-09-661-468-37
16	29	74.4	41	1	US-08-480-784-84
17	29	74.4	41	1	US-08-483-553-84
18	29	74.4	41	1	US-08-487-002-84
19	29	74.4	41	1	US-08-483-554B-84
20	29	74.4	41	1	US-08-488-011B-84
21	29	74.4	41	1	US-08-850-727-84
22	29	74.4	41	5	PCT-US95-10202-84
23	29	74.4	41	5	PCT-US95-10203-84
24	29	74.4	41	5	PCT-US95-10220-84
25	29	74.4	42	1	US-08-480-784-85
26	29	74.4	42	1	US-08-483-553-85
27	29	74.4	42	1	US-08-487-002-85

28	29	74.4	42	1	US-08-483-554B-85	Sequence 85, Appl
29	29	74.4	42	1	US-08-488-011B-85	Sequence 85, Appl
30	29	74.4	42	4	US-08-850-727-85	Sequence 85, Appl
31	29	74.4	42	5	PCT-US95-10202-85	Sequence 85, Appl
32	29	74.4	42	5	PCT-US95-10203-85	Sequence 85, Appl
33	29	74.4	42	5	PCT-US95-10220-85	Sequence 85, Appl
34	29	74.4	46	1	US-08-331-394-11	Sequence 11, Appl
35	29	74.4	46	1	US-08-250-858-11	Sequence 11, Appl
36	29	74.4	46	1	US-08-446-915-11	Sequence 11, Appl
37	29	74.4	46	2	US-08-744-139-11	Sequence 11, Appl
38	29	74.4	46	5	PCT-US95-06639-11	Sequence 11, Appl
39	29	74.4	47	1	US-08-331-394-13	Sequence 13, Appl
40	29	74.4	47	1	US-08-250-858-13	Sequence 13, Appl
41	29	74.4	47	1	US-08-446-915-13	Sequence 13, Appl
42	29	74.4	47	2	US-08-744-139-13	Sequence 13, Appl
43	29	74.4	47	2	US-08-691-814B-13	Sequence 13, Appl
44	29	74.4	47	5	PCT-US95-06639-13	Sequence 13, Appl
45	29	74.4	48	4	US-09-052-089A-13	Sequence 13, Appl

ALIGNMENTS

RESULT 1  
US-08-084-848A-3  
; Sequence 3, Application US/0804848A  
; Patent No. 5432155  
; GENERAL INFORMATION:  
; APPLICANT: Olivera, Baldomero M.  
; APPLICANT: Rivier, Jean E. F.  
; APPLICANT: Cruz, Lourdes J.  
; APPLICANT: Abogadie, Fe  
; APPLICANT: Hopkins, Chris E.  
; APPLICANT: Dykelt, John  
; APPLICANT: Torres, Josep L.  
; TITLE OF INVENTION: Conotoxins I  
; NUMBER OF SEQUENCES: 13  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Fitch, Even, Tabin & Flannery  
; STREET: 135 South LaSalle Street, Suite 900  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60603  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/084,848A  
; FILING DATE: June 29, 1993  
; CLASSIFICATION: 536  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Schumann, James J.  
; REGISTRATION NUMBER: 20856  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (619)552-1311  
; TELEFAX: (619)552-0095  
; TELEX: 20 6566 PATLAW CGO  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 amino acids  
; TYPE: amino acid  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide  
; US-08-084-848A-3  
Query Match 76.9%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
1 1111  
Db 6 NAACPXC 12

## RESULT 2

US-08-458-499-3  
Sequence 3, Application US/08458499  
Patent No. 5700778  
GENERAL INFORMATION:  
APPLICANT: Olivera, Baldomero M.  
APPLICANT: Rivier, Jean E. F.  
APPLICANT: Cruz, Lourdes J.  
APPLICANT: Abogadie, Fe  
APPLICANT: Hopkins, Chris E.  
APPLICANT: Dykert, John  
APPLICANT: Torres, Josep L.  
TITLE OF INVENTION: Conotoxins I  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fitch, Even, Tabin & Flannery  
STREET: 135 South LaSalle Street, Suite 900  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/458,499  
FILING DATE: 02-JUN-1995  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/084,848  
FILING DATE: June 29, 1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Schumann, James J.  
REGISTRATION NUMBER: 20856  
REFERENCE/DOCKET NUMBER: 52511  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619)552-1311  
TELEFAX: (619)552-0095  
TELEX: 20 6566 PATLAW CGO  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 amino acids  
TYPE: amino acid  
TOPOLOGY: unknown  
MOLECULE TYPE: peptide  
US-08-458-499-3

Query Match 76.9%; Score 30; DB 1; Length 19;  
Best Local Similarity 71.4%; Pred. No. 37;  
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NXXCPXC 10  
1 1111  
Db 6 NAACPXC 12

## RESULT 3

US-09-227-357-154  
Sequence 154, Application US/09227357  
Patent No. 6342581  
GENERAL INFORMATION:  
APPLICANT: Fischet et al.  
TITLE OF INVENTION: 123 Human Secreted Proteins  
FILE REFERENCE: P2010P1  
CURRENT APPLICATION NUMBER: US/09/227,357  
CURRENT FILING DATE: 1999-01-08

EARLIER APPLICATION NUMBER: PCT/US98/13684  
EARLIER FILING DATE: 1998-07-07  
EARLIER APPLICATION NUMBER: 60/051,926  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,793  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,925  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,929  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,803  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,732  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,931  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,932  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,916  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,930  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,918  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,920  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,733  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/052,795  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,919  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/051,928  
EARLIER FILING DATE: 1997-07-08  
EARLIER APPLICATION NUMBER: 60/055,722  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,723  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,948  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,949  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,953  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,950  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,947  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,964  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/056,360  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,684  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,984  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/055,954  
EARLIER FILING DATE: 1997-08-18  
EARLIER APPLICATION NUMBER: 60/058,785  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,664  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,660  
EARLIER FILING DATE: 1997-09-12  
EARLIER APPLICATION NUMBER: 60/058,661  
EARLIER FILING DATE: 1997-09-12  
NUMBER OF SEQ ID NOS: 672  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 154  
LENGTH: 237  
TYPE: PRT  
ORGANISM: Homo sapiens  
FEATURE:

NAME/KEY: SITE  
LOCATION: (137)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
FEATURE:  
NAME/KEY: SITE  
LOCATION: (151)  
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
US-09-227-357-154

Query Match 76.9%; Score 30; DB 4; Length 237;  
Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 122 NACCPAC 128

## RESULT 4

US-08-560-398-12  
Sequence 12, Application US/08560398  
Patent No. 5907082

GENERAL INFORMATION:  
APPLICANT: O'Neill, Sharmen  
ATTORNEY/AGENT INFORMATION:  
TITLE OF INVENTION: Ovule-Specific Gene Expression  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,398  
FILING DATE: 17-NOV-1995

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-0633000US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 12:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 718 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-560-398-12

Query Match 76.9%; Score 30; DB 2; Length 718;  
Best Local Similarity 57.1%; Pred. No. 4.9e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 105 NACCPAC 111

## RESULT 5

US-08-560-398-2  
Sequence 2, Application US/08560398  
Patent No. 5907082

GENERAL INFORMATION:  
APPLICANT: O'Neill, Sharmen

APPLICANT: Nadeau, Jeanette  
TITLE OF INVENTION: Ovule-Specific Gene Expression  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/560,398  
FILING DATE: 17-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Bastian, Kevin L.  
REGISTRATION NUMBER: 34,774  
REFERENCE/DOCKET NUMBER: 023070-0633000US

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 768 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-560-398-2

Query Match 76.9%; Score 30; DB 2; Length 768;  
Best Local Similarity 57.1%; Pred. No. 5.2e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NXXCPXC 10  
DB 176 NACCPAC 182

## RESULT 6

US-08-820-170A-34  
Sequence 34, Application US/08820170A  
Patent No. 5831058

GENERAL INFORMATION:  
APPLICANT: Tsutomu, FUJIMURA  
ATTORNEY/AGENT INFORMATION:  
APPLICANT: Takeshi, MATANABE  
APPLICANT: Masato, HORIE  
APPLICANT: Toyomasa, KATAGIRI  
TITLE OF INVENTION: HUMAN GENE  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sughrue, Mion, Zimm, Macpeak & Seas  
STREET: 2100 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: D.C.  
COUNTRY: United States  
ZIP: 20037-3202

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/820,170A  
FILING DATE:  
CLASSIFICATION: 536  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 293-7060  
TELEFAX: (202) 293-7860

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;
;   TELEX: 6491103
;   INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 810 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
;
US-08-820-170A-34

Query Match
Best Local Similarity 76.9%; Score 30; DB 2; Length 810;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10
Db 224 NHTCPTC 230

RESULT 7
US-09-055-699-34
; Sequence 34, Application US/09055699
; Patent No. 6005088
;
; GENERAL INFORMATION:
;   APPLICANT: Tsutomu, FUJIMURA
;   APPLICANT: Takeshi, WATANABE
;   APPLICANT: Masato, HORIE
;   APPLICANT: Toyomasa, KATAGIRI
;   TITLE OF INVENTION: HUMAN GENE
;   NUMBER OF SEQUENCES: 42
;   CORRESPONDENCE ADDRESSES:
;   ADDRESSEE: Sugitue, Mion, Zinn, Macpeak & Seas
;   STREET: 2100 Pennsylvania Avenue, N.W.
;   CITY: Washington
;   STATE: D.C.
;   COUNTRY: United States
;   ZIP: 20037-3202
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: Patentin Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/055,699
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: 08/820,170
;   FILING DATE:
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 293-7060
;   TELEFAX: (202) 293-7860
;   TELEX: 6491103
;   INFORMATION FOR SEQ ID NO: 34:
;   SEQUENCE CHARACTERISTICS:
;       LENGTH: 810 amino acids
;       TYPE: amino acid
;       TOPOLOGY: linear
;   MOLECULE TYPE: protein
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US-09-055-699-34

Query Match
Best Local Similarity 76.9%; Score 30; DB 3; Length 810;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10
Db 224 NHTCPTC 230

RESULT 8
US-09-273-565-34
; Sequence 34, Application US/09273565A
; Patent No. 6166190
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;
;   GENERAL INFORMATION:
;   APPLICANT: FUJIMURA, TSUTOMU
;   APPLICANT: WATANABE, TAKESHI
;   APPLICANT: HORIE, MASATO
;   TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
;   SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
;   FILE REFERENCE: Q-53599
;   CURRENT APPLICATION NUMBER: US/09/273,565A
;   CURRENT FILING DATE: 1999-03-22
;   EARLIER APPLICATION NUMBER: 09/055,699
;   EARLIER FILING DATE: 1998-04-07
;   EARLIER APPLICATION NUMBER: 08/820,170
;   EARLIER FILING DATE: 1997-03-19
;   EARLIER APPLICATION NUMBER: JP 63410/1996
;   EARLIER FILING DATE: 1996-03-19
;   EARLIER APPLICATION NUMBER: JP 69163/1997
;   EARLIER FILING DATE: 1997-03-05
;   NUMBER OF SEQ ID NOS: 95
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 34
;   LENGTH: 810
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-09-565-538-34

Query Match
Best Local Similarity 76.9%; Score 30; DB 4; Length 810;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10
Db 224 NHTCPTC 230

RESULT 9
US-09-565-538-34
; Sequence 34, Application US/09565538
; Patent No. 6333404
;
; GENERAL INFORMATION:
;   APPLICANT: FUJIMURA, TSUTOMU
;   APPLICANT: WATANABE, TAKESHI
;   APPLICANT: HORIE, MASATO
;   TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
;   SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
;   FILE REFERENCE: Q-53599
;   CURRENT APPLICATION NUMBER: US/09/565,538
;   CURRENT FILING DATE: 2000-05-05
;   PRIOR APPLICATION NUMBER: 09/273,565
;   PRIOR FILING DATE: 1999-03-22
;   PRIOR APPLICATION NUMBER: 09/055,699
;   PRIOR FILING DATE: 1998-04-07
;   PRIOR APPLICATION NUMBER: 08/820,170
;   PRIOR FILING DATE: 1997-03-19
;   PRIOR APPLICATION NUMBER: JP 63410/1996
;   PRIOR FILING DATE: 1996-03-19
;   PRIOR APPLICATION NUMBER: JP 69163/1997
;   PRIOR FILING DATE: 1997-03-05
;   NUMBER OF SEQ ID NOS: 95
;   SOFTWARE: Patentin Ver. 2.1
;   SEQ ID NO 34
;   LENGTH: 810
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;
US-09-565-538-34

Query Match
Best Local Similarity 76.9%; Score 30; DB 4; Length 810;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPCX 10
Db 224 NHTCPTC 230
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RESULT 10
US-09-661-468-34
; Sequence 34, Application US/09661468
; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; TITLE OF INVENTION: SKELETAL MUSCLE-SPECIFIC UBIQUITIN-CONJUGATING ENZYME
; FILE REFERENCE: 0-53599
; CURRENT APPLICATION NUMBER: US/09/661,468
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 34
; LENGTH: 810
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-34

Query Match
Best Local Similarity 76.9%; Score 30; DB 4; Length 810;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 224 NRTCPYC 230

RESULT 11
US-08-820-170A-37
; Sequence 37, Application US/08820170A
; Patent No. 5831058
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/820,170A
; FILING DATE:
; CLASSIFICATION: 536
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
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; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-820-170A-37

Query Match
Best Local Similarity 76.9%; Score 30; DB 2; Length 816;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 225 NRTCPYC 231

RESULT 12
US-09-055-699-37
; Sequence 37, Application US/09055699
; Patent No. 6005088
; GENERAL INFORMATION:
; APPLICANT: Tsutomu, FUJIWARA
; APPLICANT: Takeshi, WATANABE
; APPLICANT: Masato, HORIE
; APPLICANT: Toyomasa, KATAGIRI
; TITLE OF INVENTION: HUMAN GENE
; NUMBER OF SEQUENCES: 42
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
; STREET: 2100 Pennsylvania Avenue, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: United States
; ZIP: 20037-3202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/055,699
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/820,170
; FILING DATE:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; TELEX: 6491103
; INFORMATION FOR SEQ ID NO: 37:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 816 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-055-699-37

Query Match
Best Local Similarity 76.9%; Score 30; DB 3; Length 816;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 NXXCPXC 10
DB 225 NRTCPYC 231

RESULT 13
US-09-273-565-37
; Sequence 37, Application US/09273565A
; Patent No. 6166190
; GENERAL INFORMATION:
; APPLICANT: FUJIWARA, TSUTOMU
; APPLICANT: WATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
```

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; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/273,565A
; EARLIER APPLICATION NUMBER: 09/055,699
; EARLIER FILING DATE: 1998-04-07
; EARLIER APPLICATION NUMBER: 08/820,170
; EARLIER FILING DATE: 1997-03-19
; EARLIER APPLICATION NUMBER: JP 63410/1996
; EARLIER FILING DATE: 1996-03-19
; EARLIER APPLICATION NUMBER: JP 69163/1997
; EARLIER FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-273-565-37
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Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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OY 4 NXXCPCX 10
    | | |
Db 225 NRTCPTC 231
```

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RESULT 14
US-09-565-538-37
; Sequence 37, Application US/09565538
; Patent No. 6333404
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: MATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/565,538
; CURRENT FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 09/273,565
; PRIOR FILING DATE: 1999-03-22
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-565-538-37
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```
Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 4 NXXCPCX 10
    | | |
Db 225 NRTCPTC 231
```

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RESULT 15
US-09-661-468-37
; Sequence 37, Application US/09661468
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; Patent No. 6376189
; GENERAL INFORMATION:
; APPLICANT: FUJIMURA, TSUTOMU
; APPLICANT: MATANABE, TAKESHI
; APPLICANT: HORIE, MASATO
; TITLE OF INVENTION: AN ISOLATED NUCLEIC ACID MOLECULE ENCODING HUMAN
; FILE REFERENCE: O-53599
; CURRENT APPLICATION NUMBER: US/09/661,468
; CURRENT FILING DATE: 2000-09-13
; PRIOR APPLICATION NUMBER: 09/055,699
; PRIOR FILING DATE: 1998-04-07
; PRIOR APPLICATION NUMBER: 08/820,170
; PRIOR FILING DATE: 1997-03-19
; PRIOR APPLICATION NUMBER: JP 63410/1996
; PRIOR FILING DATE: 1996-03-19
; PRIOR APPLICATION NUMBER: JP 69163/1997
; PRIOR FILING DATE: 1997-03-05
; NUMBER OF SEQ ID NOS: 95
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 37
; LENGTH: 816
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-661-468-37
```

```
Query Match          76.9%: Score 30; DB 4; Length 816;
Best Local Similarity 57.1%: Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
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```
OY 4 NXXCPCX 10
    | | |
Db 225 NRTCPTC 231
```

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Search completed: December 13, 2002, 08:45:19
Job time : 3.69325 secs
```



XX WPI: 2002-106308/14.  
 DR N-PSDB; ABN17351.  
 XX  
 PT Novel human polypeptides and polynucleotides useful for diagnosing,  
 PT preventing and treating cardiovascular disease, neurodegenerative,  
 PT hyperproliferative disorders and autoimmune disorders -  
 XX  
 PS Disclosure; SEQ ID 3180; 1037Pp; English.  
 XX  
 CC The present invention describes substantially purified human proteins  
 CC (referred to as open reading frame, ORFX, where x is 1-11491 (see Table 1  
 CC in the specification). ABN15762 to ABN27252 encode the human ORFX  
 CC proteins given in ABP00010 to ABP11500. ORFX proteins are useful for  
 CC treating or preventing a pathology associated with an ORFX-associated  
 CC disorder in humans, and in the manufacture of a medicament for treating a  
 CC syndrome associated with ORFX-associated disorder. ORFX polynucleotide  
 CC sequences can be used in gene therapy. ORFX sequences can be used in the  
 CC treatment of cancer, hyperproliferative disorders, cirrhosis of liver,  
 CC psoriasis, benign tumors, keloid, degenerative disorders, haemorrhage,  
 CC osteoarthritis, neurodegenerative disorders, disorders related to organ  
 CC transplantation, cardiovascular diseases, diabetes mellitus, systemic  
 CC lupus erythematosus, hypertension, hypothyroidism, cholesterol ester  
 CC storage disease, various immune deficiencies and disorders, infectious  
 CC diseases, autoimmune disorders such as multiple sclerosis, rheumatoid  
 CC arthritis, autoimmune thyroiditis, myasthenia gravis, graft-versus-host  
 CC disease and autoimmune inflammatory eye disease. ORFX proteins are also  
 CC useful for treating burns, incisions, ulcers, for treating osteoporosis,  
 CC bone degenerative disorders, or periodontal disease, and for gut  
 CC protection or regeneration and treatment of lung or liver fibrosis,  
 CC reperfusion injury in various tissues and conditions resulting from  
 CC systemic cytokine damage.  
 CC N.B. The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic format directly from WIPO  
 CC at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 SQ Sequence 80 AA;  
 QY  
 Db Query Match 79.5%; Score 31; DB 23; Length 80;  
 Best Local Similarity 57.1%; Pred. No. 2.2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPC 10  
 1 1 1 1  
 56 NSSCPTC 62  
 Db  
 RESULT 2  
 AAG03183  
 ID AAG03183 standard; Protein; 84 AA.  
 XX  
 AC AAG03183;  
 XX  
 DT 06-OCT-2000 (first entry)  
 XX  
 DE Human secreted protein, SEQ ID NO: 7264.  
 XX  
 DE Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;  
 KM gene therapy; chromosome mapping.  
 XX  
 OS Homo sapiens.  
 XX  
 PN EP1033401-A2.  
 XX  
 PD 06-SEP-2000.  
 XX  
 PF 21-FEB-2000; 2000EP-0200610.  
 XX  
 PR 26-FEB-1999; 99US-0122487.  
 XX  
 PA (GEST ) GENSET.  
 XX  
 PI Dumas Milne Edwards J, Duclert A, Giordano J;

XX WPI: 2000-500381/45.  
 DR N-PSDB; AAC03189.  
 XX  
 PT New nucleic acid that is a 5' expressed sequence tag (5' EST) for  
 PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for  
 PT diagnostic, forensic, gene therapy and chromosome mapping procedures -  
 XX  
 PS Claim 13; SEQ ID 7264; 71Pp + CD-ROM; English.  
 XX  
 CC The present sequence is a polypeptide encoded by one of a large number  
 CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs  
 CC were prepared from total human RNAs or polyA+ RNAs derived from 30  
 CC different tissues. EST sequences usually correspond mainly to the 3'  
 CC untranslated region (UTR) of the mRNA because they are often obtained  
 CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for  
 CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in  
 CC those cases where longer cDNA sequences have been obtained, the full 5'  
 CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'  
 CC ends and can therefore be used to obtain full length cDNAs and genomic  
 CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and  
 CC chromosome mapping procedures. They are used to obtain upstream  
 CC regulatory sequences and to design expression and secretion vectors.  
 CC  
 SQ Sequence 84 AA;  
 QY  
 Db Query Match 76.9%; Score 30; DB 21; Length 84;  
 Best Local Similarity 57.1%; Pred. No. 3.2e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPC 10  
 1 1 1 1  
 20 NSQCPC 26  
 Db  
 RESULT 3  
 AAM80051  
 ID AAM80051 standard; Protein; 118 AA.  
 XX  
 AC AAM80051;  
 XX  
 DT 06-NOV-2001 (first entry)  
 XX  
 DE Human protein SEQ ID NO 3697.  
 XX  
 DE Human: cytokine; cell proliferation; cell differentiation; gene therapy;  
 KM vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;  
 KM nervous system disorder; arthritis; inflammation.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200157190-A2.  
 XX  
 PD 09-AUG-2001.  
 XX  
 PF 05-FEB-2001; 2001WO-US04098.  
 XX  
 PR 03-FEB-2000; 2000US-0496914.  
 PR 27-APR-2000; 2000US-0560875.  
 PR 20-JUN-2000; 2000US-0598075.  
 PR 19-JUL-2000; 2000US-0620335.  
 PR 01-SEP-2000; 2000US-0654936.  
 PR 15-SEP-2000; 2000US-0663561.  
 PR 20-OCT-2000; 2000US-0693325.  
 PR 30-NOV-2000; 2000US-0728422.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,  
 PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,  
 PI Xue AJ, Yang Y, Wejrtman T, Goodrich R;

DR WPI: 2001-476283/51.  
 DR N-PSDB: AAK53184.  
 XX  
 PT Nucleic acids encoding polypeptides with cytokine-like activities,  
 useful in diagnosis and gene therapy -  
 XX  
 PI  
 PS Claim 20; Page 414; 6221pp; English.  
 XX  
 CC The invention relates to polynucleotides (AAK51456-AAK53435) and the  
 CC encoded polypeptides (AAW8323-AAW80302) that exhibit activity elating to  
 CC cytokine, cell proliferation or cell differentiation or which may induce  
 CC production of other cytokines in other cell populations. The  
 CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
 CC peptide therapy. The polypeptides have various cytokine-like activities,  
 CC e.g. stem cell growth factor activity, haematopoiesis regulating  
 CC activity, tissue growth factor activity, immunomodulatory activity and  
 CC activin/inhibin activity and may be useful in the diagnosis and/or  
 CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
 CC inflammation.  
 CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666  
 CC (AAW80020) are omitted as the relevant pages from the sequence listing  
 CC were missing at the time of publication.  
 CC  
 XX  
 SQ Sequence 118 AA:  
 Query Match 76.9%; Score 30; DB 22; Length 118;  
 Best Local Similarity 57.1%; Pred. No. 4.1e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 28 NNTCPXC 34  
 XX  
 DE Human secreted protein encoded by gene 70.  
 XX  
 KW Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO931117-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 17-DEC-1998; 98WO-US27059.  
 XX  
 PR 19-DEC-1997; 97US-0068369.  
 PR 18-DEC-1997; 97US-0068006.  
 PR 18-DEC-1997; 97US-0068007.  
 PR 18-DEC-1997; 97US-0068008.  
 PR 18-DEC-1997; 97US-0068053.  
 PR 18-DEC-1997; 97US-0068054.  
 PR 18-DEC-1997; 97US-0068057.  
 PR 18-DEC-1997; 97US-0068064.  
 PR 18-DEC-1997; 97US-0070923.  
 PR 19-DEC-1997; 97US-0068169.  
 PR 19-DEC-1997; 97US-0068365.  
 PR 19-DEC-1997; 97US-0068367.  
 PR 19-DEC-1997; 97US-0068368.  
 XX

PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Carter KC, Duan RD, Feng P, Ferrie AM, Florence C;  
 PI Florence K, Greene JM, Janat F, Kyaw H, Moore PA;  
 PI Ni J, Rosen CA, Ruben SM, Shi Y, Soppet DR, Wei Y,  
 PI Yu G;  
 XX  
 DR WPI: 1999-418749/35.  
 DR N-PSDB: AAX97985.  
 XX  
 PT New isolated human genes encoding secreted polypeptides  
 XX  
 PS Claim 11; Page 383; 537pp; English.  
 XX  
 CC AAX97916 to AAX98029 represent 110 isolated human secreted protein  
 CC genes. AAX96224 to AAX96727 represent the secreted proteins encoded by  
 CC the 110 human genes. The genes and their corresponding secreted  
 CC polypeptides are useful for preventing, treating or ameliorating medical  
 CC conditions, e.g. by protein or gene therapy. Also pathological conditions  
 CC can be diagnosed by determining the amount of the new polypeptides in a  
 CC sample or by determining the presence of mutations in the new genes.  
 CC Specific uses are described for each of the 110 genes, based on which  
 CC tissues they are most highly expressed in, and include developing  
 CC products for the diagnosis or treatment of cancer, tumours, developmental  
 CC abnormalities and foetal deficiencies, blood disorders, diseases of the  
 CC immune system, autoimmune diseases, inflammation, allergies, Alzheimer's  
 CC and cognitive disorders, schizophrenia, arthritis, asthma, psoriasis,  
 CC sepsis, skin disorders, atherosclerosis, diabetes, cardiovascular  
 CC disorders, kidney disorders, digestive/endocrine disorders, infections  
 CC and AIDS. The polypeptides are also useful for identifying their binding  
 CC partners. The sequences given in AAX97907 to AAX97915 and AAX96223 are  
 CC used in the exemplification of the present invention.  
 CC  
 XX  
 SQ Sequence 130 AA:  
 Query Match 76.9%; Score 30; DB 20; Length 130;  
 Best Local Similarity 57.1%; Pred. No. 4.4e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 32 NSSCPXC 38  
 XX  
 DE Human secreted protein encoded by gene 70.  
 XX  
 KW Human; secreted protein; cancer; tumour; developmental abnormality;  
 KW foetal deficiency; blood disorder; immune system disorder; inflammation;  
 KW autoimmune disease; allergy; Alzheimer's disease; cognitive disorder;  
 KW schizophrenia; arthritis; asthma; psoriasis; sepsis; skin disorder;  
 KW atherosclerosis; diabetes; cardiovascular disorder; kidney disorder;  
 KW digestive disorder; endocrine disorder; infection; AIDS.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200114553-A1.  
 XX  
 PD 01-MAR-2001.  
 XX  
 PF 23-AUG-2000; 2000WO-NZ00166.  
 PR 23-AUG-1999; 99US-0150330.  
 XX  
 PA (GENE-) GENESIS RES & DEV CORP LTD.  
 PA (NZPA-) NEW ZEALAND PASTORAL AGRIC RES INST LTD.  
 XX  
 PI Havukkala IU, Gleen M, Grigor MR, Molenaar AJ;  
 PI WPI: 2001-226619/23.  
 DR  
 XX

PT New polypeptides and polynucleotides encoding the polypeptides, which  
PT are expressed in bovine mammary gland tissue, useful for stimulating  
PT mammary gland growth or function, or inducing differentiation of milk  
PT producing cells  
XX  
XX Claim 11; Page 64; 97pp; English.  
XX  
CC The present invention relates to proteins derived from bovine  
CC mammary gland cells. The invention is useful for stimulating  
CC bovine mammary gland cell growth and function, inhibiting the  
CC growth of various mammary gland cancer cells, inhibiting  
CC angiogenesis and vascularization of tumours, or modulating  
CC the growth of blood vessels in a mammal.  
XX  
XX Sequence 136 AA;  
OY  
Query Match 76.9%; Score 30; DB 22; Length 136;  
Best Local Similarity 57.1%; Pred. No. 4.5e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
OY 4 NXCPXC 10  
Db 26 NRTCPTC 32  
RESULT 6  
AAU16336  
ID AAU16336 standard; Protein: 147 AA.  
XX  
AC AAU16336;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human novel secreted protein, Seq ID 1289.  
XX  
XX Human; immunosuppressive; antiarthritic; antihneumatic;  
XX cytoskeletal; cardiant; vasotropic; cerebroprotective; noctropic;  
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
XX vulnery; secreted protein; rheumatoid arthritis;  
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
XX cerebrovascular disorder; cerebral ischemia; angiogenesis;  
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
XX corneal infection; wound healing; epithelial cell proliferation;  
XX skin ageing; food additive; preservative; antiproliferative.  
OS Homo sapiens.  
XX  
XX  
XX WO200155322-A2.  
XX  
XX 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US01341.  
XX  
XX 31-JAN-2000; 2000US-0179065.  
XX 04-FEB-2000; 2000US-0180628.  
XX 24-FEB-2000; 2000US-0184664.  
XX 02-MAR-2000; 2000US-0186350.  
XX 16-MAR-2000; 2000US-0189874.  
XX 17-MAR-2000; 2000US-0190076.  
XX 18-APR-2000; 2000US-0198123.  
XX 19-MAY-2000; 2000US-0205515.  
XX 07-JUN-2000; 2000US-0209467.  
XX 28-JUN-2000; 2000US-0214886.  
XX 30-JUN-2000; 2000US-0215135.  
XX 07-JUL-2000; 2000US-0216647.  
XX 07-JUL-2000; 2000US-0216880.  
XX 11-JUL-2000; 2000US-0217487.  
XX 11-JUL-2000; 2000US-0217496.  
XX 14-JUL-2000; 2000US-0218290.  
XX 26-JUL-2000; 2000US-0220963.  
XX 26-JUL-2000; 2000US-0220964.  
XX 14-AUG-2000; 2000US-0224518.  
XX 14-AUG-2000; 2000US-0224519.

PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 14-AUG-2000; 2000US-0226279.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0229287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 14-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 26-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 27-SEP-2000; 2000US-0235837.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236367.  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 13-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
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 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM,  
 XX  
 DR WPI: 2001-488783/53.  
 DR N-PSDB: AAS26323.  
 XX  
 PT New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives -  
 XX  
 XX Claim 11: SEQ ID NO 1289; 980pp: English.  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
 CC are also used in diagnosing a pathological condition or susceptibility  
 CC to a pathological condition. Antibodies to the proteins can also  
 CC be used in alleviating symptoms associated with the disorders and in  
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 CC immunosorbent assays (ELISA). Disorders which are diagnosed or treated  
 CC include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
 CC and ocular disorders e.g. corneal infection, and many other  
 CC disorders listed in the specification. The polypeptides can also

CC be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention.  
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 Best Local Similarity 57.1% Pred. No. 4.8e+02;  
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 DB 27 NSQCPAC 33  
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 KW Protein identification; signal transduction pathway; metabolic pathway;  
 KW hybridisation assay; genetic mapping; gene expression control; promoter;  
 KW termination sequence.  
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 OS Arabidopsis thaliana.  
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 PN EP1033405-A2.  
 PD 06-SEP-2000.  
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AC AAU16338;  
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XX Human; immunosuppressive; antiarthritic; antirheumatic;  
KW cytosolic; cardiant; vasotropic; cerebroprotective; neurotropic;  
KW neuroprotective; antibacterial; virucide; fungicide; ophthalmological;  
KW vulnary; secreted protein; rheumatoid arthritis;  
KW hyperproliferative disorder; cardiovascular disorder; cardiac arrest;  
KW cerebrovascular disorder; cerebral ischaemia; angiogenesis;  
KW nervous system disorder; Alzheimer's disease; infection; ocular disorder;  
KW corneal infection; wound healing; epithelial cell proliferation;  
KW skin ageing; food additive; preservative; antiproliferative.  
XX Homo sapiens.  
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XX MO200155322-A2.  
PD 02-AUG-2001.  
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KW	cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
KW	neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
KW	vulnary; secreted protein; rheumatoid arthritis;
KW	hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
KW	cerebrovascular disorder; cerebral ischemia; angiogenesis;
KW	nevous system disorder; Alzheimer's disease; infection; ocular disorder;
KW	corneal infection; wound healing; epithelial cell proliferation;
KW	skin ageing; food additive; preservative; antiproliferative.
OS	Homo sapiens.
XX	WO200155322-A2.
XX	02-AUG-2001.
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XX	31-JAN-2000; 2000US-0179065.
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PR	05-SEP-2000; 2000US-0229509.
PR	05-SEP-2000; 2000US-0229513.
PR	06-SEP-2000; 2000US-0230437.
PR	06-SEP-2000; 2000US-0230438.
PR	08-SEP-2000; 2000US-0231242.
PR	08-SEP-2000; 2000US-0231243.
PR	08-SEP-2000; 2000US-0231244.
PR	08-SEP-2000; 2000US-0231413.
PR	08-SEP-2000; 2000US-0231414.
PR	08-SEP-2000; 2000US-0232080.
PR	12-SEP-2000; 2000US-0232081.
PR	12-SEP-2000; 2000US-0231968.
PR	14-SEP-2000; 2000US-0232397.
PR	14-SEP-2000; 2000US-0232398.
PR	14-SEP-2000; 2000US-0232399.
PR	14-SEP-2000; 2000US-0232399.
PR	14-SEP-2000; 2000US-0232400.
PR	14-SEP-2000; 2000US-0232401.
PR	14-SEP-2000; 2000US-0232402.
PR	14-SEP-2000; 2000US-0232403.
PR	14-SEP-2000; 2000US-0232404.
PR	14-SEP-2000; 2000US-0232405.
PR	14-SEP-2000; 2000US-0232406.
PR	14-SEP-2000; 2000US-0232407.
PR	14-SEP-2000; 2000US-0232408.
PR	14-SEP-2000; 2000US-0232409.
PR	14-SEP-2000; 2000US-0232410.
PR	14-SEP-2000; 2000US-0232411.
PR	14-SEP-2000; 2000US-0232412.
PR	14-SEP-2000; 2000US-0232413.
PR	14-SEP-2000; 2000US-0232414.
PR	14-SEP-2000; 2000US-0232415.
PR	14-SEP-2000; 2000US-0232416.
PR	14-SEP-2000; 2000US-0232417.
PR	14-SEP-2000; 2000US-0232418.
PR	14-SEP-2000; 2000US-0232419.
PR	14-SEP-2000; 2000US-0232420.
PR	14-SEP-2000; 2000US-0232421.
PR	14-SEP-2000; 2000US-0232422.
PR	14-SEP-2000; 2000US-0232423.
PR	14-SEP-2000; 2000US-0232424.
PR	14-SEP-2000; 2000US-0232425.
PR	14-SEP-2000; 2000US-0232426.
PR	14-SEP-2000; 2000US-0232427.
PR	14-SEP-2000; 2000US-0232428.
PR	14-SEP-2000; 2000US-0232429.
PR	14-SEP-2000; 2000US-0232430.
PR	14-SEP-2000; 2000US-0232431.
PR	14-SEP-2000; 2000US-0232432.
PR	14-SEP-2000; 2000US-0232433.
PR	14-SEP-2000; 2000US-0232434.
PR	14-SEP-2000; 2000US-0232435.
PR	14-SEP-2000; 2000US-0232436.
PR	14-SEP-2000; 2000US-0232437.
PR	14-SEP-2000; 2000US-0232438.
PR	14-SEP-2000; 2

PR 05-DEC-2000; 2000US-0256719.  
 PR 06-DEC-2000; 2000US-0251479.  
 PR 08-DEC-2000; 2000US-0251856.  
 PR 08-DEC-2000; 2000US-0251868.  
 PR 08-DEC-2000; 2000US-0251869.  
 PR 08-DEC-2000; 2000US-0251989.  
 PR 08-DEC-2000; 2000US-0251990.  
 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI; 2001-488783/53.  
 DR N-PSDB; AAS25870.  
 XX  
 PT New nucleic acid molecules encoding 461 human secreted proteins for  
 PT diagnosing, preventing, treating or ameliorating medical conditions and  
 PT used as food additives or preservatives -  
 XX  
 PS Claim 11: SEQ ID NO 836; 980bp; English.  
 XX  
 CC The invention relates to isolated nucleic acid molecules and their  
 CC encoded secreted proteins. The nucleic acids and proteins are used to  
 CC prevent, treat or ameliorate a medical condition in e.g. humans, mice,  
 CC rabbits, goats, horses, cats, dogs, chickens or sheep. They  
 CC are also used in diagnosing a pathological condition or susceptibility  
 CC to a pathological condition. Antibodies to the proteins can also  
 CC be used in alleviating symptoms associated with the disorders and in  
 CC diagnostic immunoassays e.g. radioimmunoassays or enzyme linked  
 CC immunosorbant assays (ELISA). Disorders which are diagnosed or treated  
 CC include autoimmune diseases e.g. rheumatoid arthritis,  
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,  
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders  
 CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.  
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi  
 CC and ocular disorders e.g. corneal infection, and many other  
 CC disorders listed in the specification. The polypeptides can also  
 CC be used to aid wound healing and epithelial cell proliferation, to  
 CC prevent skin aging due to sunburn, to maintain organs before  
 CC transplantation, for supporting cell culture of primary tissues, to  
 CC regenerate tissues and in chemotaxis. The polypeptides can also be used  
 CC as a food additive or preservative to increase or decrease storage  
 CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,  
 CC minerals, cofactors and other nutritional components. The present  
 CC sequence represents a novel secreted protein of the invention.  
 Query Match 76.9%; Score 30; DB 22; Length 201;  
 Best Local Similarity 57.1%; Pred. No. 6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4 NXXCPXC 10  
 Db 181 NSTCPIC 187  
 RESULT 11  
 ID AAM25880  
 AC AAM25880; standard; Protein; 231 AA.  
 XX  
 DT 16-OCT-2001 (first entry)  
 XX  
 DE Human protein sequence SEQ ID NO:1395.  
 XX  
 KW Human; cancer; ulcer; HIV infection; human immunodeficiency virus;  
 KW antiinflammatory; antirheumatic; antithyritic; immunosuppressive;  
 KW antibacterial; endocrine; cardiant; central nervous system; virucide;  
 KW anti-HIV; fungicide; antimutagen; cardiovascular; antinaemic; anaemia;  
 KW antileggregant; haemostatic; vulnery; antidiacer; osteopathic; eczema;  
 KW dermatological; antiallergic; antialstmatic; antidiabetic; cyostatic;

KW neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;  
 KW immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;  
 KW antinaphylactic; rheumatoid arthritis; septic shock; pancreatitis;  
 KW genetic dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;  
 KW genetic disease; haematopoietic disorder; platelet disorder; asthma;  
 KW thrombocytopaenia; osteoporosis; severe combined immunodeficiency;  
 KW allergic rhinitis; diabetes; multiple sclerosis; depression;  
 KW Alzheimer's disease; Parkinson's disease; neurodegenerative disorder;  
 KW neurological disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200153455-A2.  
 XX  
 PD 26-JUL-2001.  
 XX  
 PF 22-DEC-2000; 2000MO-US35017.  
 XX  
 PR 23-DEC-1999; 990S-0471275.  
 PR 21-JAN-2000; 2000US-0488725.  
 PR 25-APR-2000; 2000US-0552317.  
 XX  
 PA (HYSE-) HYSEQ INC.  
 XX  
 PI Tang YT, Liu C, Drmanac RT;  
 XX  
 DR WPI; 2001-457603/49.  
 DR N-PSDB; AAH99821.  
 XX  
 PT Isolated human polynucleotides encoding polypeptides, useful for the  
 PT treatment and diagnosis of e.g. cancer, ulcers and HIV infection -  
 XX  
 PS Claim 20: Page 286; 1217bp; English.  
 XX  
 CC AAH99166 to AAH99904 encode the human proteins given in AAM25225 to  
 CC AAM25963. The proteins can have activities based on the tissues and  
 CC cells they are expressed in, such as: antiinflammatory; antithyematic;  
 CC antirheumatic; immunosuppressive; antibacterial; endocrine; cardiant;  
 CC central nervous system; virucide; anti-HIV; fungicide; antimutagen;  
 CC cardiovascular; antinaemic; antileggregant; haemostatic; vulnery;  
 CC antidiacer; osteopathic; dermatological; antiallergic; antialstmatic;  
 CC antidiabetic; cyostatic; neuroprotective; antidepressant; nootropic;  
 CC antiparkinsonian; and immunostimulant. The proteins and polynucleotides  
 CC encoding them can be used in gene therapy, antisense therapy and vaccine  
 CC production. The proteins and polynucleotides are useful for screening for  
 CC agonists or antagonists of a protein and for the treatment and diagnosis  
 CC of disorders associated with the activity of a protein e.g. inflammation,  
 CC rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction,  
 CC neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal  
 CC infections, autoimmunity, genetic diseases, haematopoietic disorders,  
 CC anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers,  
 CC osteoporosis, severe combined immunodeficiency, eczema, allergic  
 CC rhinitis, asthma, diabetes, cancer, multiple sclerosis, depression,  
 CC Alzheimer's disease, Parkinson's disease, neurodegenerative and  
 CC neurological disorders.  
 XX  
 SQ Sequence 231 AA:  
 Query Match 76.9%; Score 30; DB 22; Length 231;  
 Best Local Similarity 57.1%; Pred. No. 6.6e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 Oy 4 NXXCPXC 10  
 Db 116 NAECPCAC 122  
 RESULT 12  
 ID AAY02654  
 AC AAY02654; standard; Protein; 237 AA.  
 XX  
 AC AAY02654;

DT 11-JUN-1999 (first entry)  
 XX Human secreted protein encoded by gene 5 clone HCN5P40.  
 DE  
 XX  
 KM Human; secreted protein; fusion protein; gene therapy; protein therapy;  
 KM diagnosis; tissue; cancer; tumour; neurodegenerative disorder; leukaemia;  
 KM developmental abnormality; foetal deficiency; blood; allergy; renal;  
 KM immune system; asthma; lymphocytic disease; brain; hepatic; lymphoma;  
 KM inflammation; ischaemic shock; Alzheimer's disease; stenosis; AIDS;  
 KM cognitive disorder; schizophrenia; prostate; obesity; osteoclast; thymus;  
 KM osteoporosis; arthritis; testis; lung; thyroiditis; thyroid; digestion;  
 KM endocrine; metabolism; regulation; malabsorption; gastritis; neoplasm.  
 OS Homo sapiens.  
 XX  
 XX WO9902546-A1.  
 PN 21-JAN-1999.  
 PD  
 XX  
 PF 07-JUL-1998; 98WO-US13684.  
 XX  
 XX 12-SEP-1997; 97US-0058785.  
 PR 08-JUL-1997; 97US-0051916.  
 PR 08-JUL-1997; 97US-0051918.  
 PR 08-JUL-1997; 97US-0051919.  
 PR 08-JUL-1997; 97US-0051920.  
 PR 08-JUL-1997; 97US-0051925.  
 PR 08-JUL-1997; 97US-0051926.  
 PR 08-JUL-1997; 97US-0051928.  
 PR 08-JUL-1997; 97US-0051929.  
 PR 08-JUL-1997; 97US-0051930.  
 PR 08-JUL-1997; 97US-0051931.  
 PR 08-JUL-1997; 97US-0051932.  
 PR 08-JUL-1997; 97US-0052732.  
 PR 08-JUL-1997; 97US-0052733.  
 PR 08-JUL-1997; 97US-0052793.  
 PR 08-JUL-1997; 97US-0052795.  
 PR 08-JUL-1997; 97US-0052803.  
 PR 18-AUG-1997; 97US-0055684.  
 PR 18-AUG-1997; 97US-0055722.  
 PR 18-AUG-1997; 97US-0055723.  
 PR 18-AUG-1997; 97US-0055947.  
 PR 18-AUG-1997; 97US-0055948.  
 PR 18-AUG-1997; 97US-0055949.  
 PR 18-AUG-1997; 97US-0055950.  
 PR 18-AUG-1997; 97US-0055953.  
 PR 18-AUG-1997; 97US-0055954.  
 PR 18-AUG-1997; 97US-0055964.  
 PR 18-AUG-1997; 97US-0055984.  
 PR 18-AUG-1997; 97US-0056360.  
 PR 12-SEP-1997; 97US-0058660.  
 PR 12-SEP-1997; 97US-0058661.  
 PR 12-SEP-1997; 97US-0058664.  
 XX  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 PI Brewer LA, Ehner R, Fischer CL, Kyaw H, Lafleur DM, Li Y, Moore PA;  
 PI Olsen HS, Rosen CA, Ruben SM, Shi Y, Soppet DR, Zeng Z;  
 XX  
 DR WPI: 1999-120770/10.  
 DR N-PSDB: AAX27315.  
 XX  
 PT New isolated human genes and the secreted polypeptides they encode -  
 PT useful for diagnosis and treatment of e.g. cancers, neurological  
 PT disorders, immune diseases, inflammation or blood disorders  
 XX  
 XX Claim 11: Page 322; 464pp; English.  
 PS  
 CC This sequence represents a secreted human protein encoded by the gene  
 CC clone detailed in the descriptor line. The gene can be used to generate  
 CC fusion proteins by linking to the gene to a human immunoglobulin Fc  
 CC portion (e.g. AAX27302) for increasing the stability of the fused  
 CC protein as compared to the human protein only.

CC The invention relates to 123 novel genes and their fragments (nucleic  
 CC acid sequences: AAX27311-X27449; amino acid sequences AA02650-Y02789)  
 CC which are useful for preventing, treating or ameliorating medical  
 CC conditions e.g. by protein or gene therapy. Also, pathological  
 CC conditions can be diagnosed by determining the amount of the new  
 CC polypeptides in a sample or by determining the presence of mutations in  
 CC the new polynucleotides. Specific uses are described for each of the 123  
 CC polynucleotides, based on which tissues they are most highly expressed in  
 CC (see AAX27311 for described uses).  
 XX  
 SO Sequence 237 AA;  
 Query Match 76.9%; Score 30; DB 20; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 OY 4 NXXCPXC 10  
 DB 122 NAECPAC 128  
 RESULT 13  
 AAY87321  
 ID AAY87321 standard; Protein; 237 AA.  
 XX  
 XX AAY87321;  
 AC  
 XX  
 XX 11-MAY-2000 (first entry)  
 DT  
 XX  
 XX Human signal peptide containing protein HSP98 SEQ ID NO:98.  
 DE  
 XX  
 XX Human; signal peptide-containing protein; HSP; diagnosis; cancer;  
 KM inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KM antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;  
 KM antiasthmatic; gene therapy; cell proliferation; neurological disorder;  
 KM reproductive disorder; developmental disorder; arteriosclerosis;  
 KM cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KM asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KM Parkinson's disease; Huntington's diseases; ovulatory defect;  
 KM muscular dystrophy.  
 KM  
 OS Homo sapiens.  
 XX  
 OS  
 XX WO200000610-A2.  
 PN  
 XX  
 PD 06-JAN-2000.  
 XX  
 XX 25-JUN-1999; 99WO-US14484.  
 PF  
 XX  
 PR 26-JUN-1998; 98US-0090762.  
 PR 31-JUL-1998; 98US-0094983.  
 PR 01-OCT-1998; 98US-0102686.  
 PR 11-DEC-1998; 98US-0112129.  
 XX  
 XX (INCY-) INCYTE PHARM INC.  
 PA  
 XX  
 PI Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
 PI Akerblom LE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
 PI Bandman O;  
 XX  
 DR WPI: 2000-160673/14.  
 DR N-PSDB: AA298206.  
 XX  
 PT New human signal peptide-containing proteins useful in treatment,  
 PT prevention and diagnosis of e.g. cancer, inflammation and  
 PT cardiovascular disease  
 XX  
 XX Claim 1: Page 223; 327pp; English.  
 PS  
 XX AA298109 to AA298242 encode AAY87324 to AAY87357 which represent the  
 CC human signal peptide-containing proteins HSP98-1 to HSP98-134. HSPs have  
 CC anticancer, anti-inflammatory, antimicrobial, nootropic, hepatotropic,  
 CC neuroprotective, cardiovascular and antiasthmatic activities, and can

CC be used in gene therapy. HSPPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSPP. Antagonists of  
CC HSPP are used to treat or prevent disorders associated with increased  
CC activity or function of HSPP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis), acquired immune deficiency syndrome, anemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP  
CC nucleic acids can be used for the recombinant production of HSPP, for  
CC detecting HSPP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring). In gene therapy, as antisense,  
CC triplex-forming or ribozyme therapeutics, for detecting related sequences  
CC or genetic variations, and for chromosomal mapping. HSPP are also used to  
CC raise specific antibodies (Ab) and to screen for agonists and  
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or  
CC monitor, HSPP-related diseases (in usual immunoassays), as therapeutic  
CC antagonists, in competitive drug screens, and for purification of HSPP  
CC from natural sources.

XX Sequence 237 AA;

Query Match 76.9%; Score 30; DB 21; Length 237;  
Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 4 NXXCPC 10  
| | | |  
Db 122 NAECPAC 128

## RESULT 14

AAV6721  
ID AAV6721 standard; protein: 237 AA.

XX AAV6721;

XX 05-APR-2000 (first entry)

XX Membrane-bound protein PRO511.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

PN W09963088-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99MO-US12252.

XX 02-JUN-1998; 98US-0087607.

XX 02-JUN-1998; 98US-0087609.

XX 02-JUN-1998; 98US-0087759.

XX 03-JUN-1998; 98US-0087827.

XX 04-JUN-1998; 98US-0088021.

XX 04-JUN-1998; 98US-0088025.

XX 04-JUN-1998; 98US-0088028.

XX 04-JUN-1998; 98US-0088029.

XX 04-JUN-1998; 98US-0088030.

XX 04-JUN-1998; 98US-0088033.

XX 05-JUN-1998; 98US-0088167.

XX 05-JUN-1998; 98US-0088202.

XX 05-JUN-1998; 98US-0088212.

XX 09-JUN-1998; 98US-0088655.

XX 10-JUN-1998; 98US-0088722.

XX 10-JUN-1998; 98US-0088730.

XX 10-JUN-1998; 98US-0088734.

XX 10-JUN-1998; 98US-0088738.

PR 10-JUN-1998; 98US-0088740.  
PR 10-JUN-1998; 98US-0088741.  
PR 10-JUN-1998; 98US-0088742.  
PR 10-JUN-1998; 98US-0088810.  
PR 10-JUN-1998; 98US-0088811.  
PR 10-JUN-1998; 98US-0088824.  
PR 10-JUN-1998; 98US-0088825.  
PR 10-JUN-1998; 98US-0088826.  
PR 11-JUN-1998; 98US-0088858.  
PR 11-JUN-1998; 98US-0088861.  
PR 11-JUN-1998; 98US-0088863.  
PR 11-JUN-1998; 98US-0088876.  
PR 12-JUN-1998; 98US-0089090.  
PR 12-JUN-1998; 98US-0089105.  
PR 16-JUN-1998; 98US-0089440.  
PR 16-JUN-1998; 98US-0089512.  
PR 16-JUN-1998; 98US-0089514.  
PR 17-JUN-1998; 98US-0089532.  
PR 17-JUN-1998; 98US-0089538.  
PR 17-JUN-1998; 98US-0089598.  
PR 17-JUN-1998; 98US-0089599.  
PR 17-JUN-1998; 98US-0089600.  
PR 17-JUN-1998; 98US-0089653.  
PR 18-JUN-1998; 98US-0089601.  
PR 18-JUN-1998; 98US-0089907.  
PR 18-JUN-1998; 98US-0089908.  
PR 19-JUN-1998; 98US-0089947.  
PR 19-JUN-1998; 98US-0089948.  
PR 19-JUN-1998; 98US-0089952.  
PR 22-JUN-1998; 98US-0090246.  
PR 22-JUN-1998; 98US-0090252.  
PR 22-JUN-1998; 98US-0090254.  
PR 23-JUN-1998; 98US-0090349.  
PR 23-JUN-1998; 98US-0090355.  
PR 24-JUN-1998; 98US-0090429.  
PR 24-JUN-1998; 98US-0090431.  
PR 24-JUN-1998; 98US-0090435.  
PR 24-JUN-1998; 98US-0090444.  
PR 24-JUN-1998; 98US-0090445.  
PR 24-JUN-1998; 98US-0090472.  
PR 24-JUN-1998; 98US-0090535.  
PR 24-JUN-1998; 98US-0090538.  
PR 24-JUN-1998; 98US-0090540.  
PR 24-JUN-1998; 98US-0090557.  
PR 25-JUN-1998; 98US-0090576.  
PR 25-JUN-1998; 98US-0090678.  
PR 25-JUN-1998; 98US-0090688.  
PR 25-JUN-1998; 98US-0090690.  
PR 25-JUN-1998; 98US-0090691.  
PR 25-JUN-1998; 98US-0090694.  
PR 25-JUN-1998; 98US-0090695.  
PR 25-JUN-1998; 98US-0090696.  
PR 26-JUN-1998; 98US-0090862.  
PR 26-JUN-1998; 98US-0090863.  
PR 01-JUL-1998; 98US-0091358.  
PR 01-JUL-1998; 98US-0091360.  
PR 01-JUL-1998; 98US-0091544.  
PR 02-JUL-1998; 98US-0091478.  
PR 02-JUL-1998; 98US-0091486.  
PR 02-JUL-1998; 98US-0091519.  
PR 02-JUL-1998; 98US-0091626.  
PR 02-JUL-1998; 98US-0091628.  
PR 02-JUL-1998; 98US-0091633.  
PR 02-JUL-1998; 98US-0091646.  
PR 02-JUL-1998; 98US-0091673.  
PR 07-JUL-1998; 98US-0091978.  
PR 07-JUL-1998; 98US-0091982.  
PR 09-JUL-1998; 98US-0092182.  
PR 10-JUL-1998; 98US-0092472.  
PR 20-JUL-1998; 98US-0093339.  
PR 30-JUL-1998; 98US-0094651.  
PR 04-AUG-1998; 98US-0095282.

PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX  
 PA (GETH ) GENENTECH INC.  
 XX  
 PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;  
 XX  
 DR WPI: 2000-072883/06.  
 DR N-PSDB; AAZ65061.  
 XX  
 PT Membrane-bound proteins and related nucleotide sequences -  
 PT  
 PS claim 12; Fig 212; 822pp; English.  
 XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences  
 CC will also be useful for the preparation of PRO polypeptides, especially  
 CC by recombinant techniques.  
 CC  
 XX  
 SQ Sequence 237 AA;

Query Match 76.9%; Score 30; DB 21; Length 237;  
 Best Local Similarity 57.1%; Pred. No. 6.7e+02;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
 QY 4 NXXCPXC 10  
 Db 122 NAECPAC 128  
 RESULT 15  
 AAU29134  
 ID AAU29134 standard; Protein; 237 AA.  
 XX  
 AC AAU29134;  
 XX  
 DT 18-DEC-2001 (first entry)  
 XX  
 DE Human PRO polypeptide sequence #111.  
 XX  
 KW PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep;  
 KW dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha;  
 KW blood; chondrocyte cell; cell proliferation; cell differentiation; colon;  
 KW adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200168848-A2.  
 XX  
 PD 20-SEP-2001.  
 XX  
 PF 28-FEB-2001; 2001WO-US06520.  
 XX  
 PR 01-MAR-2000; 2000WO-US05601.  
 PR 02-MAR-2000; 2000WO-US05841.  
 PR 03-MAR-2000; 2000US-187202P.  
 PR 06-MAR-2000; 2000US-186968P.  
 PR 14-MAR-2000; 2000US-189320P.  
 PR 14-MAR-2000; 2000US-189328P.  
 PR 15-MAR-2000; 2000WO-US06884.  
 PR 21-MAR-2000; 2000US-190828P.  
 PR 21-MAR-2000; 2000US-191007P.  
 PR 21-MAR-2000; 2000US-191048P.  
 PR 21-MAR-2000; 2000US-191314P.  
 PR 28-MAR-2000; 2000US-192655P.  
 PR 29-MAR-2000; 2000US-193032P.  
 PR 29-MAR-2000; 2000US-193053P.  
 PR 30-MAR-2000; 2000WO-US08439.  
 PR 04-APR-2000; 2000US-194449P.  
 PR 11-APR-2000; 2000US-194647P.  
 PR 11-APR-2000; 2000US-195975P.  
 PR 11-APR-2000; 2000US-196000P.  
 PR 11-APR-2000; 2000US-196187P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 11-APR-2000; 2000US-196690P.  
 PR 18-APR-2000; 2000US-198121P.  
 PR 18-APR-2000; 2000US-198585P.  
 PR 25-APR-2000; 2000US-199397P.  
 PR 25-APR-2000; 2000US-199550P.  
 PR 25-APR-2000; 2000US-199654P.  
 PR 03-MAY-2000; 2000US-201516P.  
 PR 17-MAY-2000; 2000WO-US13705.  
 PR 22-MAY-2000; 2000WO-US14042.  
 PR 30-MAY-2000; 2000WO-US14941.  
 PR 02-JUN-2000; 2000WO-US15264.  
 PR 05-JUN-2000; 2000US-209832P.  
 PR 28-JUL-2000; 2000WO-US20710.  
 PR 22-AUG-2000; 2000US-0644848.  
 PR 24-AUG-2000; 2000WO-US23328.  
 PR 08-NOV-2000; 2000WO-US30952.  
 PR 01-DEC-2000; 2000WO-US32678.  
 PR 20-DEC-2000; 2000WO-US34956.  
 XX  
 PA (GETH ) GENENTECH INC.

XX Baker KP, Chen J, Desnoyers L, Goddard A, Godowski PJ, Gurney AL;  
PI Pan J, Smith V, Watanabe CK, Wood WI, Zhang Z;  
XX  
XX WPI: 2001-602746/68.  
DR N-PSDB; AAS46035.  
XX  
XX Novel nucleic acids encoding PRO polypeptides, used to diagnose the  
PT presence of tumours, such as prostate and breast tumours, in mammals and  
PT to screen for modulators of the compounds -  
XX  
XX  
PS Claim 11; Fig 222; 774pp; English.  
XX  
XX Sequences AAU29024-AAU29328 represent PRO polypeptides of the invention.  
CC The PRO polypeptides and their associated nucleic acids can be used to  
CC detect the presence of a tumour in a mammal by comparing the level of  
CC expression of a PRO polypeptide in a test sample of cells from the animal  
CC and a control sample of normal cells, whereby a higher level of  
CC expression in the test sample indicates the presence of a tumour in the  
CC mammal. Mammals include dogs, cats, cattle, horses, sheep, pigs, goats  
CC and rabbits but are preferably human. The polypeptides can be used to  
CC stimulate tumour necrosis factor (TNF) alpha release from human blood,  
CC when contacted with it. A specific polypeptide can be used to stimulate  
CC the proliferation or differentiation of chondrocyte cells. The PRO  
CC proteins can be used to determine the presence of tumours and also  
CC susceptibility to tumour development, particularly adrenal, lung, colon,  
CC breast, prostate, rectal, cervical, or liver tumours, in mammalian  
CC subjects. The oligonucleotide probes specific for the PRO nucleic acids  
CC can be used for genetic analysis of individuals with genetic disorders.  
XX  
SQ Sequence 237 AA;  
  
Query Match 76.9%; Score 30; DB 22; Length 237;  
Best Local Similarity 57.1%; Pred. No. 6,7e+02;  
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;  
  
QY 4 NXXCPXC 10  
| | |  
| | |  
Db 122 NAECPAC 128

Search completed: December 13, 2002, 08:38:13  
Job time : 5.63804 secs



GenCore version 5.1.3  
Copyright (c) 1993 - 2002 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 13, 2002, 08:39:46 ; Search time 14.8221 Seconds  
(without alignments)  
169.748 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFDDPQERPKLPOLCTELQ.....WTGRGMSCCRSSRRRTETQL 151

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105981 seqs, 16662342 residues

Total number of hits satisfying chosen parameters: 105981

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published\_Applications\_AA:\*  
1: /cgn2\_6/ptodata/2/pubpaa/US08\_NEM\_PUB pep:\*  
2: /cgn2\_6/ptodata/2/pubpaa/PC1\_NEM\_PUB pep:\*  
3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEM\_PUB pep:\*  
4: /cgn2\_6/ptodata/2/pubpaa/US06\_PUBCOMB pep:\*  
5: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:\*  
6: /cgn2\_6/ptodata/2/pubpaa/US07\_PUBCOMB pep:\*  
7: /cgn2\_6/ptodata/2/pubpaa/PC1US\_PUBCOMB pep:\*  
8: /cgn2\_6/ptodata/2/pubpaa/US08\_PUBCOMB pep:\*  
9: /cgn2\_6/ptodata/2/pubpaa/US09\_NEM\_PUB pep:\*  
10: /cgn2\_6/ptodata/2/pubpaa/US09\_PUBCOMB pep:\*  
11: /cgn2\_6/ptodata/2/pubpaa/US10\_NEM\_PUB pep:\*  
12: /cgn2\_6/ptodata/2/pubpaa/US10\_PUBCOMB pep:\*  
13: /cgn2\_6/ptodata/2/pubpaa/US60\_NEM\_PUB pep:\*  
14: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	273	9	US-10-000-903-4
2	843	99.1	292	9	US-10-000-903-10
3	843	99.1	371	9	US-10-000-903-6
4	843	99.1	390	9	US-10-000-903-14
5	469.5	55.2	278	9	US-10-000-903-21
6	469.5	55.2	383	9	US-10-000-903-23
7	80.5	9.5	256	10	US-09-756-186-2
8	78.5	9.2	552	10	US-09-764-898-183
9	78.5	9.2	553	10	US-09-764-898-163
10	78.5	9.2	4636	10	US-09-835-996A-33
11	77.5	9.1	181	10	US-09-970-532-4
12	77.5	9.1	471	10	US-09-970-532-2
13	77	9.0	285	10	US-09-756-186-6
14	76.5	9.0	162	10	US-09-798-789-18
15	76	8.9	276	10	US-09-764-864-925
16	76	8.9	468	10	US-09-864-761-37991
17	74.5	8.8	153	10	US-09-800-909-3
18	74.5	8.8	153	10	US-09-884-987-4
19	74.5	8.8	153	10	US-09-800-908-12

20	74.5	8.8	161	9	US-09-898-234-4	Sequence 4, Appli
21	74.5	8.8	161	9	US-09-899-429A-4	Sequence 4, Appli
22	74.5	8.8	161	9	US-09-797-356-4	Sequence 4, Appli
23	74.5	8.8	161	10	US-09-899-422-4	Sequence 4, Appli
24	74.5	8.8	161	10	US-09-907-263-2	Sequence 2, Appli
25	74.5	8.8	162	9	US-09-899-429A-6	Sequence 2, Appli
26	74.5	8.8	162	10	US-09-798-789-9	Sequence 2, Appli
27	74.5	8.8	162	10	US-09-798-789-22	Sequence 2, Appli
28	74.5	8.8	172	9	US-09-899-429A-10	Sequence 20, Appli
29	74.5	8.8	173	9	US-09-899-429A-16	Sequence 16, Appli
30	74.5	8.8	183	9	US-09-899-429A-10	Sequence 10, Appli
31	74.5	8.8	190	9	US-09-899-429A-18	Sequence 18, Appli
32	74.5	8.8	200	9	US-09-899-429A-12	Sequence 12, Appli
33	74.5	8.8	201	9	US-09-899-429A-14	Sequence 14, Appli
34	74.5	8.8	211	9	US-09-899-429A-8	Sequence 8, Appli
35	74.5	8.8	336	10	US-09-756-186-8	Sequence 8, Appli
36	74.5	8.8	371	9	US-09-898-234-12	Sequence 12, Appli
37	74.5	8.8	371	10	US-09-792-356-12	Sequence 12, Appli
38	74.5	8.8	371	10	US-09-899-422-12	Sequence 12, Appli
39	74.5	8.8	455	9	US-09-898-234-17	Sequence 2, Appli
40	74.5	8.8	455	9	US-09-756-854-5	Sequence 17, Appli
41	74.5	8.8	455	9	US-09-899-429A-2	Sequence 5, Appli
42	74.5	8.8	455	9	US-09-899-429A-27	Sequence 2, Appli
43	74.5	8.8	455	9	US-10-041-574-5	Sequence 27, Appli
44	74.5	8.8	455	9	US-09-792-356-2	Sequence 5, Appli
45	74.5	8.8	455	9	US-09-792-356-2	Sequence 2, Appli

#### ALIGNMENTS

RESULT 1  
US-10-000-903-4  
; Sequence 4, Application US/10000903  
; Publication No. US20020182221A1  
; GENERAL INFORMATION:  
; APPLICANT: Bruck, Claudine  
; APPLICANT: Cabazon Silva, Teresa  
; APPLICANT: Delisse, Anne-Marie Eva Fernandez  
; APPLICANT: Gerard, Catherine Marie Ghislaine  
; APPLICANT: Lombardo-Bencheikh, Angela  
; TITLE OF INVENTION: Vaccine  
; FILE REFERENCE: B45107  
; CURRENT APPLICATION NUMBER: US/10/000,903  
; CURRENT FILING DATE: 2001-10-01  
; PRIOR APPLICATION NUMBER: PCT/EP98/05285  
; PRIOR FILING DATE: 1998-08-17  
; PRIOR APPLICATION NUMBER: GB 9717953.5  
; PRIOR FILING DATE: 1997-08-22  
; NUMBER OF SEQ ID NOS: 23  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 4  
; LENGTH: 273  
; TYPE: PRT  
; ORGANISM: Homo sapien  
US-10-000-903-4  
Query Match 99.1%; Score 843; DB 9; Length 273;  
Best Local Similarity 99.3%; Pred. No. 4.3e-79;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFDDPQERPKLPOLCTELQTHIHILIECYCKQKOLLREYVDFAFRLCTIVYRGNGY 60  
DB 114 MFDDPQERPKLPOLCTELQTHIHILIECYCKQKOLLREYVDFAFRLCTIVYRGNGY 173  
QY 61 AVCDKCLKYKSYSEYRHCYSLYGTLEBOQYNNKPLCDLILRCINCKPLCEPKORHLD 120  
DB 174 AVCDKCLKYKSYSEYRHCYSLYGTLEBOQYNNKPLCDLILRCINCKPLCEPKORHLD 233  
QY 121 KQRFHINIRGRTGRCMSCCRSSRRRTETQL 151  
DB 234 KQRFHINIRGRTGRCMSCCRSSRRRTETQL 264

```
RESULT 2
US-10-000-903-10
; Sequence 10, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 292
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-10
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Query Match          99.1%; Score 843; DB 9; Length 292;
Best Local Similarity 99.3%; Pred. No. 4,6e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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```
QY 1 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 60
    |||||||
DB 133 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 192
    |||||||
QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120
    |||||||
DB 193 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 252
    |||||||
QY 121 KQRFNIRGRWTGRCMSCCRSSRTRETOL 151
    |||||||
DB 253 KQRFNIRGRWTGRCMSCCRSSRTRETOL 283
    |||||||
```

```
RESULT 3
US-10-000-903-6
; Sequence 6, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 371
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-6
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```
Query Match          99.1%; Score 843; DB 9; Length 371;
Best Local Similarity 99.3%; Pred. No. 6e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 60
    |||||||
DB 114 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 173
    |||||||
QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120
    |||||||
DB 174 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 233
    |||||||
QY 121 KQRFNIRGRWTGRCMSCCRSSRTRETOL 151
    |||||||
DB 234 KQRFNIRGRWTGRCMSCCRSSRTRETOL 264
    |||||||
```

```
RESULT 4
US-10-000-903-14
; Sequence 14, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
; PRIOR APPLICATION NUMBER: GB 9717953.5
; PRIOR FILING DATE: 1997-08-22
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-000-903-14
```

```
Query Match          99.1%; Score 843; DB 9; Length 390;
Best Local Similarity 99.3%; Pred. No. 6,4e-79;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 60
    |||||||
DB 133 MFDDPQERPRKLPOLCTELQTTIHDIILECVYCKQOLLREYVDFAFRDLCIYRDGNPY 192
    |||||||
QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120
    |||||||
DB 193 AVCDKCLKFKYSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 252
    |||||||
QY 121 KQRFNIRGRWTGRCMSCCRSSRTRETOL 151
    |||||||
DB 253 KQRFNIRGRWTGRCMSCCRSSRTRETOL 283
    |||||||
```

```
RESULT 5
US-10-000-903-21
; Sequence 21, Application US/10000903
; Publication No. US20020182221A1
; GENERAL INFORMATION:
; APPLICANT: Bruck, Claudine
; APPLICANT: Cabezon Silva, Teresa
; APPLICANT: Delisse, Anne-Marie Eva Fernandez
; APPLICANT: Gerard, Catherine Marie Ghislaine
; APPLICANT: Lombardo-Bencheikh, Angela
; TITLE OF INVENTION: Vaccine
; FILE REFERENCE: B45107
; CURRENT APPLICATION NUMBER: US/10/000,903
; CURRENT FILING DATE: 2001-10-01
; PRIOR APPLICATION NUMBER: PCT/EP98/05285
; PRIOR FILING DATE: 1998-08-17
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PRIOR APPLICATION NUMBER: GB 9717953.5  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 21  
 LENGTH: 278  
 TYPE: PRN  
 ORGANISM: Homo sapien  
 US-10-000-903-21

Query Match 55.2%; Score 469.5; DB 9; Length 278;  
 Best Local Similarity 56.1%; Pred. No. 6.8e-41;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FDDPDRPKRLPOLCTELTTHIDITLLECYCKQOLLRREYVDFARFDCIYRDSNPYA 61  
 DB 115 FEDPTRRPKRLPOLCTELTTHIDITLLECYCKQOLLRREYVDFARFDCIYRDSNPYA 174  
 QY 62 VCDKCLKFSKYSEYRHYCYSLVGTTLLEQYNNKPLCDLLIRNCINCOKPLCPPEKORHLDK 121  
 DB 175 ACHKCIDFYSRIRELHYSDSYGDTLEKLTNGLYNLIRLCRCOKPLNPAEKLAHLNE 234  
 QY 122 KORFNIRGRWTRGCMSCCRSSR-----TRRETQL 151  
 DB 235 KRRFNIIAGHYRGCHSCCNRAOERLQRRRETQV 269

RESULT 6  
 US-10-000-903-23  
 Sequence 23, Application US/10000903  
 Publication No. US2002018221A1  
 GENERAL INFORMATION:  
 APPLICANT: Bruck, Claudine  
 APPLICANT: Cabazon Silva, Teresa  
 APPLICANT: Delisse, Anne-Marie Eva Bernande  
 APPLICANT: Gerard, Catherine Marie Ghislaine  
 APPLICANT: Lombardo-Bencheikh, Angela  
 TITLE OF INVENTION: Vaccine  
 FILE REFERENCE: B45107  
 CURRENT APPLICATION NUMBER: US/10/000,903  
 CURRENT FILING DATE: 2001-10-01  
 PRIOR APPLICATION NUMBER: PCT/EP98/05285  
 PRIOR FILING DATE: 1998-08-17  
 PRIOR APPLICATION NUMBER: GB 9717953.5  
 PRIOR FILING DATE: 1997-08-22  
 NUMBER OF SEQ ID NOS: 23  
 SOFTWARE: FastSeq for Windows Version 3.0  
 SEQ ID NO: 23  
 LENGTH: 383  
 TYPE: PRN  
 ORGANISM: Homo sapien  
 US-10-000-903-23

Query Match 55.2%; Score 469.5; DB 9; Length 383;  
 Best Local Similarity 56.1%; Pred. No. 9.7e-41;  
 Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

QY 2 FDDPDRPKRLPOLCTELTTHIDITLLECYCKQOLLRREYVDFARFDCIYRDSNPYA 61  
 DB 115 FEDPTRRPKRLPOLCTELTTHIDITLLECYCKQOLLRREYVDFARFDCIYRDSNPYA 174  
 QY 62 VCDKCLKFSKYSEYRHYCYSLVGTTLLEQYNNKPLCDLLIRNCINCOKPLCPPEKORHLDK 121  
 DB 175 ACHKCIDFYSRIRELHYSDSYGDTLEKLTNGLYNLIRLCRCOKPLNPAEKLAHLNE 234  
 QY 122 KORFNIRGRWTRGCMSCCRSSR-----TRRETQL 151  
 DB 235 KRRFNIIAGHYRGCHSCCNRAOERLQRRRETQV 269

RESULT 7  
 US-09-756-186-2  
 Sequence 2, Application US/09756186

Patent No. US20010014333A1  
 GENERAL INFORMATION:  
 APPLICANT: Campbell, Robert K.  
 APPLICANT: Jameson, Bradford A.  
 APPLICANT: Chappel, Scott C.  
 TITLE OF INVENTION: HYBRID PROTEINS  
 NUMBER OF SEQUENCES: 22  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: BROWDY AND NEIMARK  
 STREET: 419 Seventh Street N.W., Ste. 300  
 City: Washington  
 STATE: D.C.  
 COUNTRY: USA  
 ZIP: 22207  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/756,186  
 FILING DATE:  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/804,166  
 FILING DATE:  
 CLASSIFICATION:  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Browdy, Roger L.  
 REGISTRATION NUMBER: 25,618  
 REFERENCE/DOCKET NUMBER: CAMPBELL-2A  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202) 628-5197  
 TELEFAX: (202) 737-3528  
 INFORMATION FOR SEQ ID NO: 2:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 256 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-09-756-186-2

Query Match 9.5%; Score 80.5; DB 10; Length 256;  
 Best Local Similarity 24.2%; Pred. No. 0.37;  
 Matches 37; Conservative 18; Mismatches 39; Indels 59; Gaps 10;

QY 28 LECYCKQOLLRREYVDFARFDCIYRDSNPYAVCDKCLKFSKYSEYRHYCYSLVGT 87  
 DB 82 LSCSKCRKEMGOVEI-----SSCTVDRD---TVCG-CRK-----NQRHY-----WSEN 121  
 QY 88 LEQYNNKPLC-----DILIR---CINC--OKPLCPPEKORHLDK 121  
 DB 122 LFQCFNCSLCNGTVHLSQOERKONTVCAGFFLENECVSCGAAPCPCECTL---Q 177  
 QY 122 KORFNIRGRWTRGCMSCC-----RSSRT 145  
 DB 178 ENPFESQCAPILQCMGCCFSRAIYPTPLRSKT 210

RESULT 8  
 US-09-764-898-183  
 Sequence 183, Application US/09764898  
 Patent No. US20020090673A1  
 GENERAL INFORMATION:  
 APPLICANT: Rosen et al.  
 TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 FILE REFERENCE: P1201  
 CURRENT APPLICATION NUMBER: US/09/764,898  
 CURRENT FILING DATE: 2001-01-17  
 PRIOR APPLICATION data removed - consult PALM or file wrapper  
 NUMBER OF SEQ ID NOS: 311  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 183

```
; LENGTH: 552
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-898-183

Query Match
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

9.2%; Score 78.5; DB 10; Length 552;

OY 51 C1VVRDGNPYAVC-----DKCLKFYSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 252 C1VYAGNOPYCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRIEG 306

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDRKORFHN-IRGRWTGRCMSC 139
Db 307 PKCE-VDKCVCHGCHGHCIIINK-----DSEDFICNCTNGKIASSCQLC 347

RESULT 9
US-09-764-898-163
; Sequence 163, Application US/09764898
; Patent No. US20020090673A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P201
; CURRENT APPLICATION NUMBER: US/09/764,898
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 311
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 163
; LENGTH: 553
; TYPE: PRT
; ORGANISM: Homo sapiens
; NAME/KEY: SITE
; LOCATION: (393)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-898-163

Query Match
Best Local Similarity 24.5%; Pred. No. 1.4;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

9.2%; Score 78.5; DB 10; Length 553;

OY 51 C1VVRDGNPYAVC-----DKCLKFYSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 253 C1VYAGNOPYCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRIEG 307

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDRKORFHN-IRGRWTGRCMSC 139
Db 308 PKCE-VDKCVCHGCHGHCIIINK-----DSEDFICNCTNGKIASSCQLC 348

RESULT 10
US-09-835-996A-33
; Sequence 33, Application US/09835996A
; Patent No. US20020142953A1
; GENERAL INFORMATION:
; APPLICANT: Ballinger, Dennis
; APPLICANT: Loeb, Debra
; APPLICANT: Montgomery, Julie
; APPLICANT: Tang, Y. Tom
; APPLICANT: Zhou, Ping
; APPLICANT: Goodrich, Kyle
; APPLICANT: Liu, Chenghua
; APPLICANT: Asundi, Vinod
; APPLICANT: Zhao, Qiang
; APPLICANT: Wehrman, Tom
; APPLICANT: Drmanac, Radoje
; APPLICANT: Ren, Feiyun
; APPLICANT: Qian, Xiaohu
; APPLICANT: Wang, Dunrui
```

```
; TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO LIPID METABOLISM
; FILE REFERENCE: 28110/35915A
; CURRENT APPLICATION NUMBER: US/09/835,996A
; CURRENT FILING DATE: 2001-04-16
; PRIOR APPLICATION NUMBER: US 60/197,137
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/714,936
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 09/667,298
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US 09/631,451
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 09/598,042
; PRIOR FILING DATE: 2000-06-20
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 33
; LENGTH: 4636
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-835-996A-33

Query Match
Best Local Similarity 24.5%; Pred. No. 15;
Matches 26; Conservative 11; Mismatches 42; Indels 27; Gaps 6;

9.2%; Score 78.5; DB 10; Length 4636;

OY 51 C1VVRDGNPYAVC-----DKCLKFYSKYSEYRHYCYSLYGTTL-----EQOYNK 94
Db 436 C1VYAGNOPYCHCOPETGTGRC-----QYVCHHYCVNSSECTTIGDGSVECVCPTRIEG 4390

OY 95 PLCDLLIRINCOKPLCPPEEKORHLDRKORFHN-IRGRWTGRCMSC 139
Db 4391 PKCE-VDKCVCHGCHGHCIIINK-----DSEDFICNCTNGKIASSCQLC 4431

RESULT 11
US-09-970-532-4
; Sequence 4, Application US/09970532
; Patent No. US20020076765A1
; GENERAL INFORMATION:
; APPLICANT: Taylor, J. Michael
; APPLICANT: Kehrl, Jr., Marcus
; APPLICANT: Lee, Eun-Kyung
; APPLICANT: Mwangi, Simon
; TITLE OF INVENTION: BOVINE TUMOR NECROSIS FACTOR RECEPTOR-1
; TITLE OF INVENTION: AND METHODS OF USE
; FILE REFERENCE: 08411-018001
; CURRENT APPLICATION NUMBER: US/09/970,532
; CURRENT FILING DATE: 2001-10-03
; PRIOR APPLICATION NUMBER: 09/513,007
; PRIOR FILING DATE: 2000-02-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 181
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-970-532-4

Query Match
Best Local Similarity 23.8%; Pred. No. 0.51;
Matches 31; Conservative 20; Mismatches 32; Indels 47; Gaps 10;

9.1%; Score 77.5; DB 10; Length 181;

OY 28 LECVYCKOQLBREYVFAFRDLC1VVRDGNPYAVCDKCLKFYSKYSEYRHYCYSLYGT 87
Db 71 LSCSRCDMEFVEI-----SPCVDRD-----TVCG-CRK-----NOYREY-----WGFT 110

OY 88 LEOOYNKPLCDLLIRINCOKPLCP-----EEOHRHLDRKORFHNIRGRWTGRCMSC 139
Db 111 -----GPRCLNCS--LCPNGTVNIPOERDPTICHGKMGFFLKG---ACISC 153

OY 140 --CRSSRTTR 147
```



QY 148 ETOL 151  
 Db 152 CTXL 155

## RESULT 15

US-09-764-864-925  
 ; Sequence 925, Application US/09764864  
 ; Patent No. US20020132753A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
 ; FILE REFERENCE: PT23  
 ; CURRENT APPLICATION NUMBER: US/09/764,864  
 ; CURRENT FILING DATE: 2001-01-17  
 ; Prior application data removed - consult PALM or file wrapper  
 ; NUMBER OF SEQ ID NOS: 1792  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 925  
 ; LENGTH: 276  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; FEATURE:  
 ; NAME/KEY: SITE  
 ; LOCATION: (198)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (203)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (229)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; NAME/KEY: SITE  
 ; LOCATION: (237)  
 ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids  
 ; US-09-764-864-925

## Query Match

8.9%; Score 76; DB 10; Length 276;  
 Best Local Similarity 25.0%; Pred. No. 1.2;

Matches 42; Conservative 16; Mismatches 62; Indels 46; Gaps 11;

QY 3 QDPERPRKLPQ---LCTELQTTIHDI-----LECVYCKQQLRREYVDFAFRDLCI 52  
 Db 74 KSPGEKPHRCPOCGCFARKSQLTGHRIHSGEPRKCPCEGKRPLRS-----DL... 124  
 QY 53 VYR-----DGNPYAVCDKCLKFYSKYSEYRHYCYSLYGTLEBOYKRPLODLDLRINC 106  
 Db 125 -YRHQRLHTGERPYE-CTVCKKRFTFRS--HLIGHQRTHSEELY-----KCLEY 170  
 QY 107 QKPLC-PEKORHL-----DKORFHNIRGWTGRCMSCRSSRPTRE 148  
 Db 171 GKSFCHGSSLKRLKLTHTGEEKPHRCN-XGKSFRLTALTLHQRTHT 217

Search completed: December 13, 2002, 08:46:16  
 Job time : 16.8221 secs

GenCore version 5.1.3  
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## OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:20 ; Search time 48.1718 Seconds  
(without alignments)  
645.878 Million cell updates/sec

Title: US-09-701-080C-18  
Perfect score: 851  
Sequence: 1 MFQDPQERPRKLPQCTELQ.....WTGRGMSCCRSSRTTRTQL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues  
Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_21.\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	151	12	089755 human papil
2	843	99.1	161	12	0919C6 human papil
3	840	98.7	151	12	089852 human papil
4	840	98.7	158	12	09WH13 human papil
5	840	98.7	158	12	08ORD8 human papil
6	840	98.7	158	12	08ORD7 human papil
7	839	98.6	151	12	089640 human papil
8	839	98.6	151	12	09W931 human papil
9	839	98.6	158	12	08QHT0 human papil
10	838	98.5	151	12	09WMP5 human papil
11	838	98.5	158	12	08OHP5 human papil
12	837	98.4	151	12	09W8C3 human papil
13	837	98.4	161	12	0919D4 human papil
14	836	98.2	158	12	09QDh9 human papil
15	836	98.2	158	12	08ORE0 human papil
16	836	98.2	158	12	08ORD9 human papil

17	834	98.0	158	12	09QDH3 human papil
18	834	98.0	158	12	08ORD6 human papil
19	834	98.0	161	12	0919B1 human papil
20	833	97.9	151	12	089648 human papil
21	833	97.9	158	12	08ORE1 human papil
22	832	97.8	151	12	080963 human papil
23	831	97.6	151	12	09WMP4 human papil
24	829	97.4	151	12	089887 human papil
25	829	97.4	158	12	09QDH7 human papil
26	829	97.4	158	12	08ORD5 human papil
27	828	97.3	151	12	09WMP2 human papil
28	826	97.1	151	12	012335 human papil
29	826	97.1	151	12	080966 human papil
30	824	96.8	151	12	089708 human papil
31	824	96.8	158	12	08OHNO human papil
32	823	96.7	158	12	09QDH5 human papil
33	822	96.6	161	12	0919A9 human papil
34	818	96.1	151	12	09WMP3 human papil
35	817	96.0	151	12	012336 human papil
36	795	93.4	143	12	0919C4 human papil
37	794	93.3	143	12	0919B6 human papil
38	768	90.2	138	12	0919D2 human papil
39	726	85.3	130	12	0919C2 human papil
40	726	85.3	130	12	0919C0 human papil
41	724	85.1	130	12	0919B4 human papil
42	722	84.8	130	12	0919D0 human papil
43	721	84.7	130	12	0919C8 human papil
44	721	84.7	130	12	0919B8 human papil
45	594	69.8	149	12	084298 human papil

## ALIGNMENTS

RESULT 1  
089755 PRELIMINARY; PRT; 151 AA.  
AC 089755;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE Early transforming protein E6.  
GN E6.  
OS Human papillomavirus, and  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10566, 10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human papillomavirus; STRAIN=OR 6170;  
RX MEDLINE=96079021; PubMed=7494284;  
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
RA Jenison S.A.;  
RT Human papillomavirus type 16 variant lineages in United States  
RT populations characterized by nucleotide sequence analysis of the E6,  
RT L2, and L1 coding segments.";  
RT J. Virol. 69:7743-7753(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human papillomavirus; STRAIN=OR 6170;  
RX Farmer A.D.;  
RA Submitted (Aug-1995) to the EMBL/Genbank/DBD databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC SPECIES=Human papillomavirus type 16; STRAIN=AS, EA7768T, AND EA7496T;  
RX van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
RT "Analysis of Human papillomavirus type 16 E6 variants in relation to  
RT p53 codon 72 polymorphism genotype in cervical carcinogenesis.";  
RT Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.  
DR EMBL; U34111; AAA91673.1; -  
DR EMBL; U34111; AAA91658.1; -

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DR EMBL: U34121; AAA91668.1; -.
DR EMBL: U34123; AAA91670.1; -.
DR EMBL: AJ388066; CAB45124.1; -.
DR EMBL: AJ388056; CAB45104.1; -.
DR EMBL: AJ388061; CAB45114.1; -.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18334 MW; FF8F2A2FCEBA6C02 CRC64;

Query Match          99.1%; Score 843; DB 12; Length 151;
Best Local Similarity 99.3%; Pred. No. 9.4e-85;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 60
Db 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 60

QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 120
Db 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 120

QY 121 KKOEFNIRGRWGTGRMCCRSSRTRETOL 151
Db 121 KKOEFNIRGRWGTGRMCCRSSRTRETOL 151

RESULT 2
QY 0919C6 PRELIMINARY; PRT; 161 AA.
AC 0919C6;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE E6 protein (Fragment).
GN E6.
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10581;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HPV16E6C6;
RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia.";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF046597; AA01351.1; -.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
FT NON_TER 1
SQ SEQUENCE 161 AA; 19628 MW; 15D32F0F12E00460 CRC64;

Query Match          99.1%; Score 843; DB 12; Length 161;
Best Local Similarity 99.3%; Pred. No. 1e-84;
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 60
Db 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 70

QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 120
Db 71 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 130

QY 121 KKOEFNIRGRWGTGRMCCRSSRTRETOL 151
Db 131 KKOEFNIRGRWGTGRMCCRSSRTRETOL 161

RESULT 3
QY 089852 PRELIMINARY; PRT; 151 AA.
AC 089852;

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DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE Early transforming protein E6 (early transforming protein E6
DE variant).
GN E6.
OS Human papillomavirus, and
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10586, 10581;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human papillomavirus; STRAIN=OR 8987;
RX MEDLINE=96079021; Pubmed=7494284;
RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,
RA Jenison S.A.;
RT "Human papillomavirus type 16 variant lineages in United States
RT populations characterized by nucleotide sequence analysis of the E6,
RT L2, and L1 coding segments.";
RL J. Virol. 69:7743-7753(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human papillomavirus; STRAIN=OR 8987;
RA Farmer A.D.;
RL Submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human papillomavirus type 16; STRAIN=EC169GDEL;
RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,
RA Verheijen R.H., Helmerhorst T.J., Meljer C.J., Walboomers J.M.;
RT "Analysis of Human papillomavirus type 16 E6 variants in relation to
RT p53 codon 72 polymorphism genotype in cervical carcinogenesis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC SPECIES=Human papillomavirus type 16; STRAIN=XINJIANG;
RA Ma Z., Qian D., Ma J., Lin R., Ming W., Zhong Z., Zhang O., Zhang F.;
RT "Cloning and Sequencing of HPV16 E6 gene from Cervical Carcinoma
RT Biopsies in Xinjiang.";
RL Shengwu Huaxue Yu Shengwu Wuli Jinzhan 0:0-0(2001).
DR EMBL: U34134; AAA91681.1; -.
DR EMBL: U34127; AAA91674.1; -.
DR EMBL: U34133; AAA91680.1; -.
DR EMBL: AJ388069; CAB45130.1; -.
DR EMBL: AJ388057; CAB45106.1; -.
DR EMBL: AF327851; AA645940.1; -.
DR InterPro: IPR001334; E6.
DR Pfam: PF00518; E6; 1.
SQ SEQUENCE 151 AA; 18320 MW; 617D2A2FDBA8FC17 CRC64;

Query Match          98.7%; Score 840; DB 12; Length 151;
Best Local Similarity 98.7%; Pred. No. 2e-84;
Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 60
Db 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQKQQLRREVYDFAFRDLCIYRDGNPY 60

QY 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 120
Db 61 AVCDKCLKFKYSKYSEYRHYCYSLYGTLEQYNNKPLCDLLIRICNCKPLCPPEKQRRHD 120

QY 121 KKOEFNIRGRWGTGRMCCRSSRTRETOL 151

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Db 121 KKORFNHNGRWTGRCMSCRSSRTRRETOL 151

## RESULT 4

Q9WH13 PRELIMINARY; PRT; 158 AA.  
 ID Q9WH13  
 AC Q9WH13;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE Isolate 16W12E, complete genome (E6 protein).  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=16W12E;  
 RX MEDLINE=99434235; PubMed=10502513;  
 RA Flores E.R., Allen-Hoffmann B.L., Lee D., Sattler C.A., Lambert P.F.;  
 RT "Establishment of the human papillomavirus type 16 (HPV-16) life cycle  
 in an immortalized human foreskin keratinocyte cell line."  
 RL Virology 262:344-354(1999).  
 RT (2)  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=16W12E;  
 RA Flores E.R., Nelson J.H., Lambert P.F.;  
 RT Submitted (Feb-1999) to the EMBL/GenBank/DBJ databases.  
 RN (3)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-C109G;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China."  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF125673; AAD33252.1; -  
 DR EMBL: AF486322; AAL96621.1; -  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SO SEQUENCE 158 AA; 19173 MW; 9F0CF5ADDA2ED7FE CRC64;

## Query Match

Best local Similarity 98.7%; Score 840; DB 12; Length 158;

Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KKORFNHNGRWTGRCMSCRSSRTRRETOL 151  
 Db 128 KKORFNHNGRWTGRCMSCRSSRTRRETOL 158

## RESULT 5

Q8ORD8 PRELIMINARY; PRT; 158 AA.  
 ID Q8ORD8  
 AC Q8ORD8;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;

RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-G449T;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China."  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486316; AAL96621.1; -  
 SO SEQUENCE 158 AA; 19188 MW; 01FEF5B1D21A7EB CRC64;

## Query Match

Best local Similarity 98.7%; Score 840; DB 12; Length 158;

Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KKORFNHNGRWTGRCMSCRSSRTRRETOL 151  
 Db 128 KKORFNHNGRWTGRCMSCRSSRTRRETOL 158

## RESULT 6

Q8ORD7 PRELIMINARY; PRT; 158 AA.  
 ID Q8ORD7  
 AC Q8ORD7;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DE 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN (1)  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E-C442T;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China."  
 RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486318; AAL96623.1; -  
 SO SEQUENCE 158 AA; 19173 MW; 14EBF5ADCFDB3640 CRC64;

## Query Match

Best local Similarity 98.7%; Score 840; DB 12; Length 158;

Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 60  
 Db 8 MFODPQERPRKLPOLCTELQTTIHDIILCEVCYCKQOLLREYVDFAFRDLCIYRGDNPY 67  
 QY 61 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 120  
 Db 68 AVCDKCLKFSKYSERHYCYSLYGTLLLEQYKPKLDCDLIRINCOKPLCPPEKORHLD 127  
 QY 121 KKORFNHNGRWTGRCMSCRSSRTRRETOL 151  
 Db 128 KKORFNHNGRWTGRCMSCRSSRTRRETOL 158

## RESULT 7

Q89640 PRELIMINARY; PRT; 151 AA.  
 ID Q89640  
 AC Q89640;

DT 01-NOV-1996 (TReMBLrel. 01, Created)  
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE Early transforming protein E6.  
 GN E6.  
 OS Human papillomavirus.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10566;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OR 7574;  
 RX MEDLINE=96079021; Pubmed=7494284;  
 RA Yamada T., Wheeler C.M., Halpern A.L., Stewart A.C., Hildesheim A.,  
 RA Jenison S.A.;  
 RT "Human papillomavirus type 16 variant lineages in United States  
 RT populations characterized by nucleotide sequence analysis of the E6,  
 RT L2, and L1 coding segments";  
 RL J. Virol. 69:7743-7753(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-OR 7574;  
 RA Farmer A.D.;  
 RU Submitted (Aug-1995) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: U34129; AAA91676.1; -;  
 DR EMBL: U34115; AAA91662.1; -;  
 DR EMBL: U34120; AAA91667.1; -;  
 DR EMBL: U34124; AAA91671.1; -;  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18348 MW; FE3F2A2FCF0A6CB2 CRC64;

Query Match 98.6%; Score 839; DB 12; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 2.6e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 60  
 DB 1 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 60  
 QY 61 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 120  
 DB 61 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 120  
 QY 121 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 151  
 DB 121 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 151

RESULT 8  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 151 AA.  
 AC Q9W931;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-EA246T 2;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 RA Verheijen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of Human papillomavirus type 16 E6 variants in relation to  
 RT p53 codon 72 polymorphism genotype in cervical carcinogenesis";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ388059; CAB45110.1; -;  
 DR EMBL: AJ388058; CAB45108.1; -;  
 DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18306 MW; 6FB3D9E0F24A5300 CRC64;  
 Query Match 98.6%; Score 839; DB 12; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 2.6e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 60  
 DB 1 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 60  
 QY 61 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 120  
 DB 61 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 120  
 QY 121 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 151  
 DB 121 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 151

RESULT 9  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 158 AA.  
 AC Q9W931;  
 DT 01-JUN-2002 (TReMBLrel. 21, Created)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxID=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AS-P, AS-C193, AND AS-A178;  
 RA Chan P.K.-S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 RA Cheung J.L.K., Xu L.Y., Cheng A.F.;  
 RT "Human papillomavirus type 16 intra-typic variant infection and risk  
 RT for cervical neoplasia in Southern China";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486399; AAL96604.1; -;  
 DR EMBL: AF486300; AAL96605.1; -;  
 DR EMBL: AF486301; AAL96606.1; -;  
 DR EMBL: AF486302; AAL96607.1; -;  
 DR EMBL: AF486306; AAL96611.1; -;  
 DR EMBL: AF486308; AAL96613.1; -;  
 SQ SEQUENCE 158 AA; 19201 MW; 004EF5ADC6B375B CRC64;

Query Match 98.6%; Score 839; DB 12; Length 158;  
 Best Local Similarity 98.7%; Pred. No. 2.7e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 60  
 DB 8 MFQDPQERPRKLPQCLTELQTTIHDIIECYCKQOQLLRREVYDFARDLCTIVYRDGNPY 67  
 QY 61 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 120  
 DB 68 AVCCKCKLFYSKSYSEYRHYCYSLYGTLEQYKNPCLDCLIRINCQKPLCPPEKORHLD 127  
 QY 121 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 151  
 DB 128 KKQRFHNRGRWGTGRMCCSCSSRTRETQL 158

RESULT 10  
 Q9W931  
 ID Q9W931 PRELIMINARY; PRT; 151 AA.  
 AC Q9W931;  
 DT 01-NOV-1999 (TReMBLrel. 12, Created)  
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)

DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxId=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-ET182G;  
 RX MEDLINE=20112892; PubMed=10644829;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 Verheljen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of Human papillomavirus type 16 E6 variants in relation to  
 p53 codon 72 polymorphism genotypes in cervical carcinogenesis.";  
 RL J. Gen. Virol. 81:317-325(2000).  
 DR EMBL: AJ242681; CAB45381.1; -;  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18320 MW; 617D2D5FD93F8917 CRC64;

Query Match 98.5%; Score 838; DB 12; Length 151;  
 Best Local Similarity 98.0%; Pred. No. 3.3e-84;  
 Matches 148; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 |||||  
 DB 1 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 QY 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120  
 |||||  
 DB 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120  
 QY 121 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 151  
 |||||  
 DB 121 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 151

RESULT 11  
 Q80HP5 PRELIMINARY; PRT; 158 AA.  
 AC Q80HP5;  
 DT 01-JUN-2002 (TREMBLrel. 21, Created)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxId=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-E-G276T; AND E-G276G442T;  
 RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
 Cheung J.L.K., Xu L.Y., Cheng A.F.;  
 RT "Human papillomavirus type 16 intratypic variant infection and risk  
 for cervical neoplasia in Southern China.";  
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF486315; AAL96620.1; -;  
 DR EMBL: AF486323; AAL96628.1; -;  
 SQ SEQUENCE 158 AA; 19160 MW; AFF015533FC7FAF7 CRC64;

Query Match 98.5%; Score 838; DB 12; Length 158;  
 Best Local Similarity 98.7%; Pred. No. 3.5e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 |||||  
 DB 8 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 67  
 QY 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120  
 |||||  
 DB 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 127

QY 121 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 151  
 |||||  
 DB 128 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 158

RESULT 12  
 Q9W8C3 PRELIMINARY; PRT; 151 AA.  
 ID Q9W8C3;  
 AC Q9W8C3;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxId=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-AA, AND AFA7689T;  
 RA van Duin M., Snijders P.J., Vossen M.T., Klaassen E., Voorhorst F.,  
 Verheljen R.H., Helmerhorst T.J., Meijer C.J., Walboomers J.M.;  
 RT "Analysis of Human papillomavirus type 16 E6 variants in relation to  
 p53 codon 72 polymorphism genotype in cervical carcinogenesis.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AJ388064; CAB45120.1; -;  
 DR EMBL: AJ388062; CAB45116.1; -;  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 SQ SEQUENCE 151 AA; 18360 MW; FF9A2A3ADBAA7902 CRC64;

Query Match 98.4%; Score 837; DB 12; Length 151;  
 Best Local Similarity 98.7%; Pred. No. 4.3e-84;  
 Matches 149; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 |||||  
 DB 1 MFODPQERPRKLPQLCTELQTTIHDIILCEVCYCKQQLRREYVDFAFRDLCIYRDGNPY 60  
 QY 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120  
 |||||  
 DB 61 AVCDKCLKEFSKYSEYRHYCYSLYGTTLLEQYNNKPLCDLLIRINCOKPLCPPEKORHLD 120  
 QY 121 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 151  
 |||||  
 DB 121 KROFHNIRGRTGRCMSCCRSSRTTRRETOL 151

RESULT 13  
 Q919D4 PRELIMINARY; PRT; 161 AA.  
 ID Q919D4;  
 AC Q919D4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)  
 DE E6 protein (Fragment).  
 GN E6.  
 OS Human papillomavirus type 16.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 OX NCBI\_TaxId=10581;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-HPV16E6CC2;  
 RA Watts K.J., Thompson C.H., Cossart Y.E., Rose B.R.;  
 RT "Sequence variation and physical state of human papillomavirus type 16  
 cervical cancer isolates from Australia and New Caledonia.";  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF404693; AAL01343.1; -;  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.

FT NON\_TER 1 1  
SQ SEQUENCE 161 AA; 19624 MW; 10C72CDB14200460 CRC64;

Query Match 98.4%; Score 837; DB 12; Length 161;  
Best Local Similarity 98.7%; Pred. No. 4.6e-84;

Matches 149; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 60  
DB 11 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 70  
QY 61 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 120  
DB 71 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 130  
QY 121 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 151  
DB 131 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 161

## RESULT 14

Q9QDH9 PRELIMINARY; PRT; 158 AA.

AC Q9QDH9;  
DT 01-MAY-2000 (TREMBlrel. 13, Created)  
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE E6 protein.  
GN E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=KE6-1;  
RA Lee H.P., Song Y.S., Kim J.W., Roh J.W., Park N.H., Kang S.B.;  
RT "The most commonly found Human Papillomavirus type 16 E6 and E7  
sequence variation tend to occur together."  
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AS-C442;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RT "Human papillomavirus type 16 intra-typic variant infection and risk  
for cervical neoplasia in Southern China."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF187866; AAF13392.1; -;  
DR EMBL; AF486304; AAL96609.1; -;  
DR EMBL; AF486305; AAL96610.1; -;  
DR InterPro: IPR001334; E6.  
DR Pfam: PF00518; E6; 1.  
SQ SEQUENCE 158 AA; 19187 MW; 155BF5ADCEB36F0 CRC64;

Query Match 98.2%; Score 836; DB 12; Length 158;  
Best Local Similarity 98.0%; Pred. No. 5.8e-84;

Matches 148; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 60  
DB 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 67  
QY 61 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 120  
DB 68 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 127  
QY 121 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 151  
DB 128 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 158

RESULT 15, 5

Q8ORE0 PRELIMINARY; PRT; 158 AA.

AC Q8ORE0;  
DT 01-JUN-2002 (TREMBlrel. 21, Created)

DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)  
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)  
DE E6 protein.  
GN E6.  
OS Human papillomavirus type 16.  
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
OC Papillomavirus.  
OX NCBI\_TaxID=10581;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=AS-G137;  
RA Chan P.K.S., Lam C.W., Cheung T.H., Li W.W.H., Lo K.W.K., Chan M.Y.M.,  
RT "Human papillomavirus type 16 intra-typic variant infection and risk  
for cervical neoplasia in Southern China."  
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF486307; AAL96612.1; -;  
SQ SEQUENCE 158 AA; 19187 MW; 005E2FC1E617C55B CRC64;

Query Match 98.2%; Score 836; DB 12; Length 158;  
Best Local Similarity 98.0%; Pred. No. 5.8e-84;

Matches 148; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 60  
DB 8 MFODPOERPRKLPOLCTELQTTIHDIILECYCKQOQLLRREYDFAFRDLCIYRDGNPY 67  
QY 61 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 120  
DB 68 AVCDCKLFYSKYSEYRHYCYSLYGTLEQYKNPLCDLLIRINCINCOPLCPEEKORHLD 127  
QY 121 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 151  
DB 128 KKORFHNIIRGHWIGRCMSCCSSSRTRETOL 158

Search completed: December 13, 2002, 08:39:39  
Job time : 50.1718 secs

GenCore version 5.1.3  
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:31:40 ; Search time 15.7485 Seconds  
(Without alignments)  
397.685 Million cell updates/sec

Title: US-09-701-080c-18

Sequence: 1 MFQDPOERPRLKLPOLCTELQ.....WTGRCMSCRSRRTRETOL 151

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	158	1	VE6_HPVI6
2	592	69.6	149	1	VE6_HPVI3
3	538	63.2	149	1	VE6_HPVI3
4	534	62.7	149	1	VE6_HPVI3
5	516	60.6	149	1	VE6_HPVI3
6	507	59.6	148	1	VE6_HPVI3
7	499	58.6	148	1	VE6_HPVI3
8	483.5	56.8	158	1	VE6_HPVI3
9	482.5	56.7	158	1	VE6_HPVI3
10	474	55.7	151	1	VE6_HPVI3
11	473.5	55.6	158	1	VE6_HPVI3
12	469.5	55.2	158	1	VE6_HPVI3
13	465.5	54.7	158	1	VE6_HPVI3
14	463.5	54.5	158	1	VE6_HPVI3
15	454	53.3	191	1	VE6_HPVI3
16	450.5	52.9	150	1	VE6_HPVI3
17	441.5	51.9	155	1	VE6_HPVI3
18	406.5	47.8	153	1	VE6_HPVI3
19	394	46.3	154	1	VE6_HPVI3
20	387.5	45.5	155	1	VE6_HPVI3
21	342.5	40.2	155	1	VE6_HPVI3
22	322	37.8	153	1	VE6_HPVI3
23	321	37.7	150	1	VE6_HPVI3
24	320	37.6	150	1	VE6_HPVI3
25	318	37.4	150	1	VE6_HPVI3
26	316.5	37.2	153	1	VE6_HPVI3
27	315	37.0	144	1	VE6_HPVI3
28	311	36.5	159	1	VE6_HPVI3
29	310	36.4	150	1	VE6_HPVI3
30	307.5	36.1	154	1	VE6_HPVI3
31	305.5	35.9	154	1	VE6_HPVI3
32	305	35.8	150	1	VE6_HPVI3
33	300	35.3	142	1	VE6_HPVI3

34	289	34.0	150	1	VE6_HPVI3	002269 human papil
35	284	33.4	150	1	VE6_HPVI3	P27228 human papil
36	281	33.0	146	1	VE6_HPVI3	P08094 human papil
37	260	30.6	146	1	VE6_HPVI3	P50802 human papil
38	257	30.2	148	1	VE6_HPVI3	P36802 human papil
39	257	30.2	148	1	VE6_HPVI3	P50803 human papil
40	252	29.6	152	1	VE6_HPVI3	P36729 human papil
41	196.5	23.1	165	1	VE6_HPVI3	P50775 human papil
42	196	23.0	140	1	VE6_HPVI3	P00785 human papil
43	192	22.6	140	1	VE6_HPVI3	P50777 human papil
44	189.5	22.3	157	1	VE6_HPVI3	P50776 human papil
45	188.5	22.2	142	1	VE6_HPVI3	P08092 human papil

## ALIGNMENTS

RESULT 1	VE6_HPVI6	STANDARD:	PRT:	158 AA.
AC	P03126:			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	E6 protein.			
GN	E6.			
OS	Human papillomavirus type 16.			
OC	Viruses; dsDNA viruses, no RNA stage: Papillomaviridae;			
OC	Papillomavirus.			
OX	NCBI_TaxID=10581;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=65246220; PubMed=2990099;			
RA	Seedorf K., Krammer G., Durst M., Suhai S., Roweckamp W.G.;			
RT	"Human papillomavirus type 16 DNA sequence.";			
RL	Virology 145:181-185(1985).			
RN	[2]			
RP	SEQUENCE OF 31-50 FROM N.A.			
RX	MEDLINE=90218027; PubMed=2157796;			
RA	Schneider-Maunoury S., Penau-Arnaudet G., Breitburd F., Orth G.;			
RT	"Expression of the human papillomavirus type 16 genome in SK-V cells,			
RL	a line derived from a vulvar intraepithelial neoplasia.";			
CC	J. Gen. Virol. 71:809-817(1990).			
CC	-1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.			
CC	-1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE			
CC	STRANDED DNA (IN VITRO).			
CC	-1- SUBCELLULAR LOCATION: Nuclear matrix-associated.			
CC	-1- SUBCELLULAR LOCATION: HPV16, IN COMPARISON TO HPV TYPES 6 AND 11, IS MORE			
CC	OFTEN ASSOCIATED WITH MALIGNANT GENITAL CANCERS IN HUMANS.			
CC	-----			
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CC	-----			
DR	EMBL; K02718; AAA46939.1; -			
DR	EMBL; D00735; BAA00632.1; -			
DR	PIR; A03682; W6WILS.			
DR	InterPro: IPR001334; E6.			
DR	Pfam; PF00518; E6; 1.			
KW	Early protein; DNA-binding; Nuclear protein; Zinc-finger;			
FT	Oncoogene.			
FT	ZN_FING 37 73			POTENTIAL.
FT	ZN_FING 110 146			POTENTIAL.
FT	SEQUENCE 158 AA; 19187 MW; 01FE5A0CFDB37EB CRC64;			
Query Match	99.1%;	Score 843;	DB 1;	Length 158;
Best Local Similarity	99.3%;	Pred. No. 5.2e-74;		
Matches 150;	Conservative 0;	Mismatches 1;	Gaps 0;	

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
 DB 8 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 67  
 QY 61 AVCDKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 120  
 DB 68 AVCDKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 127  
 QY 121 KKRFHNINGRWTGRMCCSCRSRTRETOL 151  
 DB 128 KKRFHNINGRWTGRMCCSCRSRTRETOL 158

RESULT 2  
 VEG\_HPV35  
 ID VEG\_HPV35 STANDARD: PRT: 149 AA.  
 AC P27228:

DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE E6 protein.

OS Human papillomavirus type 35.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.

OX NCBI\_TaxID=10587;

RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=94265501; PubMed=8205838;

RA Dellus H., Hofmann B.;  
 RT Primer-directed sequencing of human papillomavirus types.;

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

RN [2]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=92124753; PubMed=1310198;

RA Marich J.E., Pontsler A.V., Rice S.M., McGraw K.A., Dubensky T.W.;

RT The phylogenetic relationship and complete nucleotide sequence of

human papillomavirus type 35.;

RL Virology 186:770-776(1992).

CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL

OF THIS VIRUS (ASSOCIATED WITH CANCER OF THE UTERINE CERVIX).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE

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CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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CC EMBL: X74477; CA52561.1; -

DR EMBL: M74117; AAA46966.1; -

DR PIR: E40824; W6WJ35.

DR PIR: S36521; S36521.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;

KW Oncogene.

FT ZN\_FING 30 66  
 FT ZN\_FING 103 139  
 SQ SEQUENCE 149 AA; 18045 MW; C605D19AF3935021 CRC64;

Query Match 69.6%; Score 592; DB 1; Length 149;  
 Best Local Similarity 71.5%; Pred. No. 5, 2e-50;  
 Matches 108; Conservative 14; Mismatches 27; Indels 2; Gaps 1;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
 DB 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60

QY 61 AVCDKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 120  
 DB 61 GVCMKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 120

QY 121 KKRFHNINGRWTGRMCCSCRSRTRETOL 151  
 DB 121 KKRFHNINGRWTGRMCCSCRSRTRETOL 151

RESULT 3  
 VEG\_HPV31  
 ID VEG\_HPV31 STANDARD: PRT: 149 AA.  
 AC P17386;

DT 01-AUG-1990 (Rel. 15, Created)  
 DT 01-AUG-1990 (Rel. 15, Last sequence update)  
 DT 15-JUN-2002 (Rel. 41, Last annotation update)  
 DE E6 protein.

OS Human papillomavirus type 31.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.

OX NCBI\_TaxID=10585;

RN [1]

RP SEQUENCE FROM N.A.  
 RX MEDLINE=89299478; PubMed=2545036;

RA Goldsborough M.D., Disilvestre D., Temple G.F., Lorincz A.T.;

RT Nucleotide sequence of human papillomavirus type 31: a cervical

neoplasia-associated virus.;

RL Virology 171:306-311(1989).

CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL

OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE

STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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CC EMBL: J04353; AAA46950.1; -

DR PIR: A32444; W6WJ31.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;

KW Oncogene.

FT ZN\_FING 30 66  
 FT ZN\_FING 103 139  
 SQ SEQUENCE 149 AA; 17713 MW; 61D2A86C362767D9 CRC64;

Query Match 63.2%; Score 538; DB 1; Length 149;  
 Best Local Similarity 65.6%; Pred. No. 7, 6e-45;  
 Matches 99; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60  
 DB 1 MFODPOERPRKLPOLCTELQTTIHDIILCEVCYCKOOLLREYVDFAFRDLCTIVYRDGNPY 60

QY 61 AVCDKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 120  
 DB 61 GVCMKCLAFYSKSEYRHYCYSLYGTTLEQOYKPKPLCDLLIRINCQKPLCEPEKORHLD 120

QY 121 KKRFHNINGRWTGRMCCSCRSRTRETOL 151  
 DB 121 KKRFHNINGRWTGRMCCSCRSRTRETOL 151

RESULT 4  
 VEG\_HPV33  
 ID VEG\_HPV33 STANDARD: PRT: 149 AA.

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AC P06427;
DR 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 33.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10586;
RN [1]
RP MEDLINE=86200464; PubMed=3009902;
RA Cole S.T., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 33, which is associated with cervical cancer.";
RL J. Virol. 58:991-995(1986).
CC -1- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL
CC OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC
CC -----
CC DR EMBL, M12732; AAA46958.1; -.
CC DR PIR, A03683; W6WL33.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger;
CC KW Oncogene.
CC FT ZN_FING 30 66 POTENTIAL.
CC FT ZN_FING 103 139 POTENTIAL.
CC SQ SEQUENCE 149 AA; 17652 MW; EDDB7444F9C8B1AF CRC64;

Query Match
Best Local Similarity 62.7%; Score 534; DB 1; Length 149;
Matches 96; Conservative 20; Mismatches 33; Indels 2; Gaps 1;

OY 1 MFDQPERRRKLPOLCTELQTHDILIECYCKQDLRREYDFAFRLDLYRRGNPY 60
DB 1 MFDTEKERTLHDLQALETTHNIELOCECKKPLQSEYVDFAFADLTYYRGNPF 60
OY 61 AVCDKCLKFKYSKYSEYRHHCYSYGTTLTLEQYNNKPLCDLLIRINCQKPLCEKORHLD 120
DB 61 GICKLCLRLSKISEYRHHCYSYGTTLTLEQYNNKPLCDLLIRINCQKPLCEKORHLD 120
OY 121 KQRFHNIGRWGTGRCMSCCRSSRTRETQL 151
DB 121 LNKRFHNIGRWGTGRCACWRP--RRRETAL 149

RESULT 5
VE6_HPV58 STANDARD; PRT; 149 AA.
AC P26555;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 58.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10598;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=92024102; PubMed=1656594;
RA Kiri Y., Iwamoto S., Matsukura T.;
RT "Human papillomavirus type 58 DNA sequence.";
RL Virology 185:424-427(1991).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC
CC -----
CC DR EMBL, D90400; BAA1845.1; -.
CC DR PIR, E36779; W6WL58.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC DR Early protein; DNA-binding; Nuclear protein; Zinc-finger.
CC KW ZN_FING 30 66 POTENTIAL.
CC FT ZN_FING 103 139 POTENTIAL.
CC SQ SEQUENCE 149 AA; 17794 MW; 79B3DC95831B158 CRC64;

Query Match
Best Local Similarity 60.6%; Score 516; DB 1; Length 149;
Matches 95; Conservative 19; Mismatches 35; Indels 2; Gaps 1;

OY 1 MFDQPERRRKLPOLCTELQTHDILIECYCKQDLRREYDFAFRLDLYRRGNPY 60
DB 1 MFDTEKERTLHDLQALETTHNIELOCECKKPLQSEYVDFAFADLTYYRGNPF 60
OY 61 AVCDKCLKFKYSKYSEYRHHCYSYGTTLTLEQYNNKPLCDLLIRINCQKPLCEKORHLD 120
DB 61 AVCKVCLRLSKISEYRHHCYSYGTTLTLEQYNNKPLCDLLIRINCQKPLCEKORHLD 120
OY 121 KQRFHNIGRWGTGRCMSCCRSSRTRETQL 151
DB 121 LNKRFHNIGRWGTGRCACWRP--RRRETQV 149

RESULT 6
VE6_HPV52 STANDARD; PRT; 148 AA.
AC P36814;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 52.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10618;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94265501; PubMed=8205838;
RA Delius H., Hofmann B.;
RT "Primer-directed sequencing of human papillomavirus types.";
RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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DR EMBL: X74481; CAAS2585.1; -.  
 DR PIR: S36573; S36573.  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 KM Early protein; DNA-binding; Nuclear protein; zinc-finger.  
 FT ZN\_FING 30 66 POTENTIAL.  
 FT ZN\_FING 103 139 POTENTIAL.  
 SQ SEQUENCE 148 AA; 17898 MW; C5E9DECE341ABDE CRC64;

Query Match 59.6%; Score 507; DB 1; Length 148;  
 Best Local Similarity 63.1%; Pred. No. 7e-42;  
 Matches 89; Conservative 18; Mismatches 34; Indels 0; Gaps 0;

QY 1 MFQDQPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFARPLCTIYRDGNPY 60  
 DB 1 MFEDPAPRPTLHCLCEVLESVEHRLQCQCKELQREVEYKFLPTDLRIYRDNNPY 60  
 QY 61 AVDCKLKFSKSEYHNYCYSLXGTLLEQYKPKLDDLIRINCOKPLCPKPKORHL 120  
 DB 61 GVCIMCRLFLSKISEYHNYCYSLXGTLLEBKVKPKLSEIRICITCOTPLCPKPKERHVN 120  
 QY 121 KQRFHNRGRTGRCMSCR 141  
 DB 121 AKRFHNRGRTGRCSECR 141

RESULT 7  
 ID V66\_HPV34 STANDARD; PRT; 148 AA.  
 AC P36811;  
 DT 01-JUN-1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 01-OCT-1994 (Rel. 30, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 34.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 NC NCBL\_TaxID=10613;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=9425501; PubMed=8205838;  
 RA Delius H., Hofmann B.,  
 RT Primer-directed sequencing of human papillomavirus types. \*;  
 RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).  
 CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE  
 CC STRANDED DNA (IN VITRO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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DR EMBL: X74476; CAAS2555.1; -.  
 DR PIR: S36515; S36515.  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 KM Early protein; DNA-binding; Nuclear protein; zinc-finger.  
 FT ZN\_FING 31 67 POTENTIAL.  
 FT ZN\_FING 104 140 POTENTIAL.  
 SQ SEQUENCE 148 AA; 17735 MW; E2FC6E62E4AFODA CRC64;

Query Match 58.6%; Score 499; DB 1; Length 148;  
 Best Local Similarity 61.1%; Pred. No. 4.1e-41;  
 Matches 88; Conservative 17; Mismatches 39; Indels 0; Gaps 0;

QY 2 FQDQPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFARPLCTIYRDGNPY 61  
 DB 3 FPNRPERPRKLPALCEVNISIHIEILDVCYCEKOLYRCEVDFIFADLCVYVRKPKLG 62

QY 62 VCDCKLKFSKSEYHNYCYSLXGTLLEQYKPKLDDLIRINCOKPLCPKPKORHL 121  
 DB 63 VQCPCLLFYSKSVGRYRNYNSVGRILENTLNQCLNILLIRGCKQKPLCPLEKQHRVDE 122  
 QY 122 KQRFHNRGRTGRCMSCR 145  
 DB 123 NKRFEHQAIDQWTRCTQCMRPSAT 146

RESULT 8  
 ID V66\_HPV70 STANDARD; PRT; 158 AA.  
 AC P50804;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 01-NOV-1997 (Rel. 35, Last annotation update)  
 DE E6 protein.  
 GN E6.  
 OS Human papillomavirus type 70.  
 OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;  
 OC Papillomavirus.  
 NC NCBL\_TaxID=39457;  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=96249586; PubMed=8815087;  
 RA Forslund O., Hansson B.G.;  
 RT "Human papillomavirus type 70 genome cloned from overlapping PCR  
 RT products: complete nucleotide sequence and genomic organization.";  
 RL J. Clin. Microbiol. 34:802-809(1996).  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE=97060129; PubMed=8904450;  
 RA Longuet M., Beaudeau S., Orth G.;  
 RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70,  
 RT related to the potentially oncogenic HPV39.";  
 RL J. Clin. Microbiol. 34:738-744(1996).  
 CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE  
 CC STRANDED DNA (IN VITRO).  
 CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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 CC -----

DR EMBL: U21941; AAC54850.1; -.  
 DR EMBL: U22461; AAC54880.1; -.  
 DR InterPro: IPR001334; E6.  
 DR Pfam: PF00518; E6; 1.  
 KM Early protein; DNA-binding; Nuclear protein; zinc-finger.  
 FT ZN\_FING 32 68 POTENTIAL.  
 FT ZN\_FING 105 141 POTENTIAL.  
 FT CONFICT 100 100 N -> D (IN REF. 2).  
 SQ SEQUENCE 158 AA; 18617 MW; 6B610800D923DDE CRC64;

Query Match 56.8%; Score 483.5; DB 1; Length 158;  
 Best Local Similarity 57.4%; Pred. No. 1.3e-39;  
 Matches 89; Conservative 21; Mismatches 40; Indels 5; Gaps 1;

QY 2 FQDQPERPRKLPOLCTELQTTIHDIILECYCKQQLLRREYDFARPLCTIYRDGNPY 61  
 DB 4 FPNRPERPRKLPALCTALDTLTDITIDCYCKTQLOQTEVEYFAFSDFIYVRNEPYA 63  
 QY 62 VCDCKLKFSKSEYHNYCYSLXGTLLEQYKPKLDDLIRINCOKPLCPKPKORHL 121  
 DB 64 ACCKCITKFAKVELKRLHNSVATITLESITNNKLVNLSRCSCLKPLCPAKLKHVN 123  
 QY 122 KQRFHNRGRTGRCMSCR 151



Db 124 KRREHOIAGSYTGOCRHCHWTSNREDRRIRRETOV 158

RESULT 9

VE6\_HP68 STANDARD; PRT; 158 AA.

AC P54667;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 01-OCT-1996 (Rel. 34, Last annotation update)

DE E6 protein.

GN E6.

OS Human papillomavirus type 68.

OC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TaxID=45240;

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=97060129; Pubmed=8904450;

RA Longuet M., Beaudeon S., Orth G.;

RT "Two novel genital human papillomavirus (HPV) types, HPV68 and HPV70, related to the potentially oncogenic HPV39."

RL J. Clin. Microbiol. 34:738-744(1996).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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CC

DR EMBL: X67160; CAA47632.1; -

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; zinc-finger.

FT ZN\_FING 32 68

FT ZN\_FING 105 141

FT ZN\_FING 158 18796 MW: 46B3793CFBA6596 CRC64;

SQ SEQUENCE 158 AA; 18796 MW; 46B3793CFBA6596 CRC64;

Query Match 56.7%; Score 482.5; DB 1; Length 158;

Best Local Similarity 55.1%; Pred. No. 1.7e-39;

Matches 86; Conservative 24; Mismatches 41; Indels 5; Gaps 1;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYDFARFDCIYRGDNPY 60

DB 3 LFHNPDEPRYKLPDLCTRLDTLHDVITIDCVYCRQQLQRTVEYEFARSDLCVYRDGPVF 62

QY 61 AVCCKCLFYSKSEYRHYCSLYGTILEQOYNKPLCDLIRINCQKPLCPCKEORHLD 120

DB 63 AACSCIKFYKIRELRYSYVATLETITNKLNLIRCMSCUKPLCPAEKRLRLT 122

QY 121 KKOFHNIRGWTGRCMCCRSS-----RTRRETOL 151

DB 123 TKRLRLKIAGNFTGOCRHCHWTSNREDRRIRRETOV 158

RESULT 10

VE6\_HP51 STANDARD; PRT; 151 AA.

AC P26534;

DT 01-AUG-1992 (Rel. 23, Created)

DT 01-AUG-1992 (Rel. 23, Last sequence update)

DT 01-JUN-1994 (Rel. 29, Last annotation update)

DE E6 protein.

GN E6.

OS Human papillomavirus type 51.

OC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TaxID=10595;

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=91303675; Pubmed=1649326;

RA Lungu O., Crum C.P., Silverstein S.J.;

RT "Biologic properties and nucleotide sequence analysis of human papillomavirus type 51."

RL J. Virol. 65:4216-4225(1991).

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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CC

DR EMBL: M62877; -; NOT\_ANNOTATED\_CDS.

DR PIR: E40415; M6M151.

DR InterPro: IPR001334; E6.

DR Pfam: PF00518; E6; 1.

KW Early protein; DNA-binding; Nuclear protein; zinc-finger.

FT ZN\_FING 30 66

FT ZN\_FING 103 139

FT ZN\_FING 151 577663BA1376478 CRC64;

SQ SEQUENCE 151 AA; 18134 MW; 577663BA1376478 CRC64;

Query Match 55.7%; Score 474; DB 1; Length 151;

Best Local Similarity 57.0%; Pred. No. 1e-38;

Matches 86; Conservative 25; Mismatches 40; Indels 0; Gaps 0;

QY 1 MFODPQRPRLPOLCTELQTTIHDIILECYCKQQLRREYDFARFDCIYRGDNPY 60

DB 1 MFEDKRRPRPLHELCLALNVSMNIIQVYCVCKELCRADYVNAATEIKIRYRDNNPY 60

QY 61 AVCCKCLFYSKSEYRHYCSLYGTILEQOYNKPLCDLIRINCQKPLCPCKEORHLD 120

DB 61 AVCCKCLFYSKIREYRYSYVGTILEATIKSLYDLSIRCHRCRPLGPEKORHLD 120

QY 121 KKOFHNIRGWTGRCMCCRSSRTRRETOL 151

DB 121 EKRFHEIAGRWGOCANCWQRTRORETOV 151

RESULT 11

VE6\_HP45 STANDARD; PRT; 158 AA.

AC P21735;

DT 01-MAY-1991 (Rel. 18, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE E6 protein.

GN E6.

OS Human papillomavirus type 45.

OC Viruses: dsDNA viruses, no RNA stage; Papillomaviridae;

OC Papillomavirus.

OX NCBI\_TaxID=10593;

RN

RP SEQUENCE FROM N.A.

RX MEDLINE=94265501; Pubmed=8205838;

RA Delius H., Hofmann B.;

RT "Primer-directed sequencing of human papillomavirus types.;"

RL Curr. Top. Microbiol. Immunol. 186:13-31(1994).

CC -1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.

CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE STRANDED DNA (IN VITRO).

CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.

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CC -----
DR EMBL; X74479; CAA52573.1; -
DR EMBL; M38198; AAA46973.1; -
DR PIR; S36561; S36561
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;
KW Oncogene.
FT ZN_FING 32 68 POTENTIAL.
FT ZN_FING 105 141
FT CONFLICT 10 10 R->P (IN REF. 2).
FT CONFLICT 30 30 I->N (IN REF. 2).
FT CONFLICT 118 118 R->A (IN REF. 2).
SQ SEQUENCE 158 AA; 18897 MW; FICF10DD33AA4C3E CRC64;

Query Match 55.6%; Score 473.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 1.2e-38;
Matches 87; Conservative 23; Mismatches 40; Indels 5; Gaps 1;

OY 2 FODPOERPRKLPOLCTELQTTIHDIIECYVCCKOQLRREYDFAFDLCIVRDGNPYA 61
DB 4 FDDPQRGRYKLPDLCTELNTSLQDYSINCYCKATLETFEYGFARFOLCIYRNCINVA 63
OY 62 VCDKCLAFYSKYSERHYCSLYGTTLLEQOYNKPLCDLLIRNCINQKPLCPBEKORHLDK 121
DB 64 ACHKCIDYYSRIRELYRSNSVGETLEKINTLEYNLLIRCLRCQKPLNPAEKRRHLKD 123

OY 122 KORFHNRGRTGRCMCCRSS-----RTREPOL 151
DB 124 KRREHNIAGHYRGCHSCCNRAQERLRRLRRRETGV 158

RESULT 12
VE6_HPVI8 STANDARD; PRT; 158 AA.
ID VE6_HPVI8
AC P06463;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6
OS Human papillomavirus type 18.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10582;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-67283882; Pubmed-3039146;
RA Cole S.T., Banos O.;
RT "Nucleotide sequence and comparative analysis of the human
RT papillomavirus type 18 genome. Phylogeny of papillomaviruses and
RT repeated structure of the E6 and E7 gene products.";
RL J. Mol. Biol. 193:599-608(1987).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-6630665; Pubmed-3018129;
RA Malatjewski G., Banks L., Wu-Liao J., Spence P., Plm D., Crawford L.;
RT "The expression of human papillomavirus type 18 E6 protein in
RT bacteria and the production of anti-E6 antibodies.";
RL J. Gen. Virol. 67:1909-1916(1986).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-88188247; Pubmed-2833614;
RA Terada M., Sugimura T.; Takebe N., Nawa H., Nakanishi S.;
RT "Nucleotide sequences of cDNAs for human papillomavirus type 18
RT transcripts in HeLa cells.";
RL J. Virol. 62:1640-1646(1988).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE-67053870; Pubmed-3023067;
RA Schneider-Gaedcke A., Schwarz E.;
RT "Different human cervical carcinoma cell lines show similar
RT transcription patterns of human papillomavirus type 18 early genes.";
RL EMO J. 5:2285-2292(1986).
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE-67218459; Pubmed-3034571;
RA Seedorf K., Oltersdorf T., Kraemer G., Roewekamp W.;
RT "Identification of early proteins of the human papilloma viruses type
RT 16 (HPV 16) and type 18 (HPV 18) in cervical carcinoma cells.";
RL EMO J. 6:139-144(1987).
RN [6]
RP ZINC-BINDING.
RX MEDLINE-69385606; Pubmed-2550872;
RA Grossman S.R., Laimins L.A.;
RT "E6 protein of human papillomavirus type 18 binds zinc.";
RL Oncogene 4:1089-1093(1989).
CC -1- FUNCTION: THIS PROTEIN HAS TRANSFORMING ACTIVITY IN VITRO.
CC -1- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC STRANDED DNA (IN VITRO).
CC -1- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
DR EMBL; X04354; CAA27879.1; -
DR EMBL; X05015; CAA28664.1; -
DR EMBL; M20325; AAA99514.1; -
DR EMBL; M26798; AAA46946.1; -
DR EMBL; X04773; CAA28466.1; -
DR EMBL; A06324; CAA00539.1; -
DR EMBL; A06328; CAA00542.1; -
DR PIR; G26251; W6WL18.
DR InterPro; IPR001334; E6.
DR Pfam; PF00518; E6; 1.
KW Early protein; DNA-binding; Nuclear protein; Zinc-finger;
KW Oncogene.
FT ZN_FING 32 68 POTENTIAL.
FT ZN_FING 105 141
FT CONFLICT 22 22 N->S (IN REF. 4).
SQ SEQUENCE 158 AA; 18871 MW; 5BCF13CF43D57FA CRC64;

Query Match 55.2%; Score 469.5; DB 1; Length 158;
Best Local Similarity 56.1%; Pred. No. 2.9e-38;
Matches 87; Conservative 22; Mismatches 41; Indels 5; Gaps 1;

OY 2 FODPOERPRKLPOLCTELQTTIHDIIECYVCCKOQLRREYDFAFDLCIVRDGNPYA 61
DB 4 FEDTTRRYKLPDLCTELNTSLQDIEITCYCKVLETFEFAFDLPFYVYDSDSPA 63
OY 62 VCDKCLAFYSKYSERHYCSLYGTTLLEQOYNKPLCDLLIRNCINQKPLCPBEKORHLDK 121
DB 64 ACHKCIDYYSRIRELYRSNSVGETLEKINTLEYNLLIRCLRCQKPLNPAEKRLHNE 123

OY 122 KORFHNRGRTGRCMCCRSS-----RTREPOL 151
DB 124 KRREHNIAGHYRGCHSCCNRAQERLRRLRRRETGV 158

RESULT 13
VE6_HPVI8 STANDARD; PRT; 158 AA.
ID VE6_HPVI8
AC P27962;
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DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type ME180.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91374616; PubMed-1716694;
RA Reuter S., Delius H., Kahn T., Hofmann B., Zur Hausen H., Schwarz E.;
RT "Characterization of a novel human papillomavirus DNA in the cervical
RT carcinoma cell line ME180."
RL J. Virol. 65:5564-5568(1991).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
CC CC
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CC -----
CC DR EMBL: M73258; -, NOT_ANNOTATED_CDS.
CC DR PIR: C40509; W6WLP.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC KM Early protein; DNA-binding; Nuclear protein; Zinc-finger.
CC FT ZN_FING 32 68 POTENTIAL.
CC FT ZN_FING 106 141 POTENTIAL.
CC SQ SEQUENCE 158 AA; 18738 MW; 2B1F406B563F05FC CRC64;

Query Match
Best Local Similarity 54.7%; Score 465.5; DB 1; Length 158;
Matches 86; Conservative 22; Mismatches 43; Indels 5; Gaps 1;

OY 1 MFQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQOQLRREVDFAFRDLCTIYRDGNPY 60
DB 3 LFHNPEERPRKLPDLCTRLDTLHDVTIDCVYCRQLQRTVEYEFAGDLNVTYRGVPL 62
OY 61 AVCDKLTFRYSKYSEYRHYCYSLYGTTLLEQYKPLCDLLIRINCQKPLCPBEKORHDK 120
DB 63 AACQSCIKFYAKIRLEIRYSESYATLTITNTKLYDLISIRQMCCLKPLSPAELKRLHN 122
OY 121 KROFHNIRGMRWTGRSCMSCCRSS-----TRRRETOL 151
DB 123 SKRRFKIAGNFTGCCRHCMTSKREDRRRLRRETQV 158

RESULT 14
VE6_HPV39
ID VE6_HPV39 STANDARD; PRT; 158 AA.
AC P24835;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE E6 protein.
GN E6.
OS Human papillomavirus type 39.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10588;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135017; PubMed-1847266;
RA Volpers C., Streeck R.E.;
RT "Genome organization and nucleotide sequence of human papillomavirus
RT type 39.";
```

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RL Virology 181:419-423(1991).
CC -!- FUNCTION: THIS PROTEIN MAY BE INVOLVED IN THE ONCOGENIC POTENTIAL
CC OF THIS VIRUS (CERVICAL NEOPLASIA-ASSOCIATED VIRUS).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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CC -----
CC DR EMBL: M62849; AAA47050.1; -.
CC DR PIR: A38502; W6WLP39.
CC DR InterPro: IPR001334; E6.
CC DR Pfam: PF00518; E6; 1.
CC KM Early protein; DNA-binding; Nuclear protein; Zinc-finger;
CC KM Oncogene.
CC FT ZN_FING 32 68 POTENTIAL.
CC FT ZN_FING 105 141 POTENTIAL.
CC SQ SEQUENCE 158 AA; 18726 MW; 1B5E9D55BC1B662E CRC64;

Query Match
Best Local Similarity 54.5%; Score 463.5; DB 1; Length 158;
Matches 86; Conservative 20; Mismatches 44; Indels 5; Gaps 1;

OY 2 FQDPQERPRKLPQLCTELQTTIHDIILCEVCYKQOQLRREVDFAFRDLCTIYRDGNPYA 61
DB 4 FHNPARPRKLPDLCTRLDTLTDIIRIACVYCRPQLQRTVEYEFAGDLNVTYRGVPLA 63
OY 62 VCDCKLFRYSKYSEYRHYCYSLYGTTLLEQYKPLCDLLIRINCQKPLCPBEKORHDK 121
DB 64 AACQSCIKFYAKIRLEIRYSESYATLTITNTKLYDLIRQMCCLKPLSPAELKRLHNS 123
OY 122 KROFHNIRGMRWTGRSCMSCCRSS-----TRRRETOL 151
DB 124 KRRFKIAGSYTGCCRHCMTSKREDRRRLRRETQV 158

RESULT 15
VE6_RHPV1
ID VE6_RHPV1 STANDARD; PRT; 191 AA.
AC P22159;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE E6 protein.
GN E6.
OS Rhesus papillomavirus type 1 (Rhpv 1).
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10570;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-91135018; PubMed-1847267;
RA Ostrow R.S., Labresh K.V., Faras A.J.;
RT "Characterization of the complete Rhpv 1 genomic sequence and an
RT integration locus from a metastatic tumor."
RL Virology 181:424-429(1991).
CC -!- FUNCTION: EXHIBIT A STRONG, BUT NON SPECIFIC AFFINITY FOR DOUBLE
CC -!- STRANDED DNA (IN VITRO).
CC -!- SUBCELLULAR LOCATION: Nuclear matrix-associated.
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OM protein - protein search, using sw model

Run on: December 13, 2002, 08:36:45 ; Search time 24.0859 Seconds

(without alignments)  
602.689 Million cell updates/sec

Title: US-09-701-080C-18

Perfect score: 851

Sequence: 1 MFQDPQERPKLPOLCTELQ.....WTGRCMSCCRSSRTTRRETQL 151

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR\_73:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	843	99.1	158	1 W6WLHS	protein E6 - human
2	592	69.6	149	1 W6WL35	E6 protein - human
3	538	63.2	149	1 W6WL31	E6 protein - human
4	534	62.7	149	1 W6WL33	E6 protein - human
5	516	60.6	149	1 W6WL58	E6 protein - human
6	507	59.6	148	2 A61237	E6 protein - human
7	507	59.6	148	2 S36573	E6 protein - human
8	499	58.6	148	2 S36515	E6 protein - human
9	474	55.7	151	1 W6WL51	E6 protein - human
10	473.5	55.6	158	2 S36561	E6 protein - human
11	469.5	55.2	158	1 W6WL18	E6 protein - human
12	465.5	54.7	158	1 W6WLPR	E6 protein - human
13	463.5	54.5	158	1 W6WL39	E6 protein - human
14	454	53.3	191	1 W6WLK1	E6 protein - human
15	450.5	52.9	150	2 S36544	E6 protein - human
16	441.5	51.9	155	1 W6WL56	E6 protein - human
17	406.5	47.8	153	2 S36503	E6 protein - human
18	394	46.3	154	2 S36527	E6 protein - human
19	387.5	45.5	155	2 A44890	E6 protein - human
20	342.5	40.2	155	2 W6WL43	E6 protein - human
21	332	37.8	153	1 S15621	E6 protein - human
22	320	37.6	150	1 W6WL6	E6 protein - human
23	318	37.4	150	1 W6WL44	E6 protein - human
24	316.5	37.2	159	2 S15614	E6 protein - human
25	311	36.5	159	2 S36497	E6 protein - human
26	310	36.4	150	1 W6WL11	E6 protein - human
27	307.5	36.1	154	2 S36584	E6 protein - human
28	305.5	35.9	154	2 S36555	E6 protein - human
29	305	35.8	150	1 W6WL1	E6 protein - human

30	300	35.3	142	2 S36509	E6 protein - human
31	289	34.0	150	1 W6WL13	E6 protein - human
32	284	33.4	150	1 W6WL42	E6 protein - human
33	257	30.2	148	2 S36532	E6 protein - human
34	252	29.6	152	2 S36550	E6 protein - human
35	182	21.4	138	2 S36567	E6 protein - human
36	170.5	20.0	141	2 S36479	E6 protein - human
37	156	18.3	156	1 W6WL41	E6 protein - human
38	155.5	18.3	140	1 W6WL	E6 protein - human
39	154	18.1	161	2 S36491	E6 protein - human
40	150.5	17.7	139	1 W6WL2	E6 protein - human
41	150.5	17.7	141	2 S36473	E6 protein - human
42	150	17.6	157	2 S36538	E6 protein - human
43	148.5	17.5	207	2 S28510	E6 protein - human
44	146	17.2	156	1 W6WL47	E6 protein - human
45	145	17.0	166	2 S36485	E6 protein - human

#### ALIGNMENTS

RESULT 1  
W6WLHS  
protein E6 - human papillomavirus type 16  
C:Species: human papillomavirus type 16  
C:Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 20-Aug-1999  
C:Accession: A03682; T10427  
R:Seedorf, K.; Kramer, G.; Durst, M.; Suhai, S.; Rowe, W. G.  
Virology 145, 181-185, 1985  
A:Title: Human papillomavirus type 16 DNA sequence.  
A:Reference number: A22355; MUID:85246220; PMID:2990099  
A:Accession: A03682  
A:Molecule type: DNA  
A:Residues: 1-158 <SEQ>  
A:Cross-references: GB:K02718; NID:9333031; PIDN:AAA46939.1; PID:9333032  
R:Kennedy, I.M.; Haddow, J.K.; Clements, J.B.  
J. Virol. 65, 2093-2097, 1991  
A:Title: A negative element in the human poapillomavirus type 16 genome acts at the 1  
A:Reference number: 217014; MUID:91162763; PMID:1848319  
A:Accession: T10427  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-158 <KEN>  
A:Cross-references: EMBL:K02718; NID:9333031; PIDN:AAA46939.1; PID:9333032  
C:Genetics:  
A:Gene: E6  
C:Superfamily: papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:37-73/Region: zinc finger CCCC motif  
F:110-146/Region: zinc finger CCCC motif

Query Match 99.1%; Score 843; DB 1; Length 158;  
Best Local Similarity 99.3%; Pred. No. 8.3e-69;  
Matches 150; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MFQDPQERPKLPOLCTELQTHDITLHCYVKKQQLRREYVDFARQDCTIVRGPNY 60  
|||||  
Db 8 MFQDPQERPKLPOLCTELQTHDITLHCYVKKQQLRREYVDFARQDCTIVRGPNY 67  
|||||

QY 61 AVQDKLKFYSKSEYRHYCYSLYGTLLDQYKRPICDLIRICINQKPLCPKPKRHH 120  
|||||  
Db 68 AVQDKLKFYSKSEYRHYCYSLYGTLLDQYKRPICDLIRICINQKPLCPKPKRHH 127  
|||||

QY 121 KKQFHNIRGWTGRCMSCCRSSRTTRRETQL 151  
|||||  
Db 128 KKQFHNIRGWTGRCMSCCRSSRTTRRETQL 158  
|||||

RESULT 2  
W6WL35  
E6 protein - human papillomavirus type 35  
C:Species: human papillomavirus type 35  
A:Note: host Homo sapiens (man)

C:Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 23-Mar-2001  
C:Accession: E040824; S36521  
R:Marich, J.E.; Pontsler, A.V.; Rice, S.M.; McGraw, K.A.; Dubensky, T.W.  
Virology 186, 770-776, 1992  
A:Title: The phylogenetic relationship and complete nucleotide sequence of human papillomavirus type 16  
A:Reference number: A40824; MUID:92124753; PMID:1310198  
A:Accession: E040824  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-149 <DNA>  
A:Cross-references: GB:W14117; NID:g333050; PIDN:AAAA46966.1; PID:g333051  
R:Delius, H.; Hofmann, B.  
submitted to the EMBL Data Library, August 1993  
A:Description: Primer-directed sequencing of human papillomavirus types.  
A:Reference number: S36469  
A:Accession: S36521  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-149 <DEL>  
A:Cross-references: EMBL:X74477; NID:g396997; PIDN:CAA52561.1; PID:g396998  
A:Experimental source: strain 35H  
C:Superfamily: papillomavirus B6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

[illegible]

RESULT 3  
W6M131  
E6 protein - human papillomavirus type 31  
C:Species: human papillomavirus type 31  
A:Note: host Homo sapiens (man)  
C:Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 16-Jul-1999  
C:Accession: A32444  
R:Goldsporough, M.D.; Dislyestre, D.; Temple, G.F.; Lorincz, A.T.  
Virology 171, 306-311, 1989  
A:Title: Nucleotide sequence of human papillomavirus type 31: a cervical neoplasia-associ  
A:Reference number: A94398; MUID:89299478; PMID:2545036  
A:Accession: A32444  
A:Status: translation not shown  
A:Molecule type: DNA  
A:Residues: 1-149 <GOI>  
A:Cross-references: GB:J04353; NID:q333048; PIDN:AAA46950.1; PID:q459916  
C:Comment: This protein may be involved in the oncogenic potential of this virus.  
C:Superfamily: Papillomavirus E6 protein  
C:Keywords: DNA binding; early protein; zinc finger  
F:30-66/Region: zinc finger CCCC motif  
F:103-139/Region: zinc finger CCCC motif

Query Match 63.2% Score 538; DB 1; Length 149;  
Best Local Similarity 65.6%; Pred. No. 2,le-41;  
Matches 99; Conservative 18; Mismatches 32; Indels 2; Gaps 1;

QY 1 MFQDQERPRKLPGLCTELTTTHIILLCVYCCKOQLRREYDFAFRDCLTYRGDNFY 60  
||||| ||||| : : | : ||||| : ||||| :  
DB 1 MEKNAPERRRKHEHSSALEITPYDELRLNVCYCKOLTELELDAFDLTIVYRDDPDPH 60

QY 61 AVKCKLKEVSKASYSHYACVSLKGTGLLEOQYNPLCDLLIPGICNOCKPLCPBEKQRHLD 120  
 Db 61 GVCITKCLFEYSKVSSEFPKRYKRSVYGTGLTEKTKNKGIDDLIRCTQGRPLCPBEKQRHLD 120  
 QY 121 KKQFHNTIKRWGTGRMSGCCSSSTRRRTQL 151  
 Db 121 KKKRHHNTGGKRWGTGRKCIACWR--RPRTETQV 149

```

RESULT 4
M6ML3
E6 protein - human papillomavirus type 33
C:Species: human papillomavirus type 33
C:Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 16-Jul-1999
C:Accession: A03683
R:Cole, S.T.; Strebeck, R.E.
J. Virol. 58, 991-995, 1986
A>Title: Genome organization and nucleotide sequence of human papillomavirus type 33.
A:Reference number: A93020; MUID:86200464; PMID:3009902
A:Accession: A03683
A:Molecule type: DNA
A:Residues: 1-149 <COL>
A:Cross-references: GB:M2732; NID:q333049; PTD:AAA46558.1; PID:q463177
C:Superfamily: Papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

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Query Match	62.7%	Score 534	DB 1	Length 149
Best Local Similarity	63.6%	Pred. Num. 4.8e-41		
Matches	96	Conservative	20	Mismatches 33; Indels 2; Gaps 1
OY	1	MFQDQERPRKRLPOLCTELQTTIHDIIILECYCCKOOLLREYVYDFAFPLDLCIVYRDGNY	60	
		:    :    :    :    :    :    :    :    :    :    :    :    :    :    :    :		
Db	1	MFQDIEERKPRTLHDLCQALFETIINHIELQVCCKKPLQSEVYVYDFAFALYVYRGNGNF	60	
OY	61	AVCDKCLAFYSKYSEYRHAYCYSLYGTLEEQYNNKPLCDLLIRCIINQKPLCEEKORHLD	120	
		:    :    :    :    :    :    :    :    :    :    :    :    :    :    :		
Db	61	GICKLCLEPLKISIEYRHNYSVYGTLEQYKPKPLNEILLIRCIICQRPCLCQEKKRHYD	120	
OY	121	KKQRFHNIRGRWTRGCMSCCRSSRRRRQQL	151	
		:    :    :    :    :    :    :    :    :    :    :    :    :    :		
Db	121	LNRKPHNISGRWAGRCACWRSS--RRRETFAL	149	

```

RESULT 5
M6WL58
E6 protein - human papillomavirus type 58
C:Species: human papillomavirus type 58
A:Note: host Homo sapiens (man)
C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 21-Jul-2000
C:Accession: E36779
R:Kiriil, Y.; Iwamoto, S.; Matsukura, T.
Virology 185, 424-427, 1991
A:Title: Human papillomavirus type 58 DNA sequence.
A:Reference number: A36779; MUID:92024102; PMID:1656594
A:Accession: E36779
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-149 <NIR>
A:Cross-references: GB:D90400; NID:G222386; PIDN:BA31845.1; PID:g3337098
C:Superfamily: papillomavirus E6 protein
C:Keywords: DNA binding; early protein; zinc finger
F:30-66/Region: zinc finger CCCC motif
F:103-139/Region: zinc finger CCCC motif

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[illegible]









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